

STIC-Biotech/ChemLib

144685

From: Bowman, Amy
Sent: Wednesday, February 09, 2005 9:04 AM
To: STIC-Biotech/ChemLib
Subject: sequence search-~~10/820,720~~ **10/820,820**

Please search SEQ ID NO: 4 in application 10/820,820, length limited to 150 nucleotides.

Thank you,
Amy Bowman
AU 1635

STAFF USE ONLY

Searcher: _____

Searcher Phone: 2-

Date Searcher Picked up: *2/16/05*

Date Completed: *2/20/05*

Searcher Prep/Rev/Time: _____

Online Time: _____

Type of Search /
NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____

DIALOG: _____

QUESTEL/ORBIT: _____

LEXIS/NEXIS: _____

SEQUENCE SYSTEM: *101* _____

WWW/Internet: _____

Other(Specify): _____

Run on: February 18, 2005, 17:58:16 ; Search time 1454 Seconds
 (without alignments)
 3165.919 Million cell updates/sec

Title: OM nucleic - nucleic search, using sw model

Perfect score: US-10-820-820-4

Sequence: 1 accgguuuguuccguagu.....aaacaaagacagucuuu 95

scoring table: IDENTITY_NUC GapOp 10_-, Gapext 1.0

searched: 470233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 2505164

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_hhg:*

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4: gb_im:*

5: gb_ov:*

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9: gb_pr:*

10: gb_ro:*

11: gb_sc:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Length	DB ID	Description
1	95	100.0	95	E33206 Expression system for functional nucleic acid transcription.
2	95	100.0	95	AX138447 Sequence
3	95	100.0	95	BD015615 Slidable
4	76.8	80.8	132	AR041184 Sequence
5	76.8	80.8	132	AR113038 Sequence
6	76.8	80.8	132	AR113038 Sequence
7	74.8	78.7	132	BD143601 Method of
8	74.8	78.7	88	BD143502 Nucleic acid synthesis
9	74.8	78.7	88	BD182356 Novel max
10	74.8	78.7	100	BD17174 Method for
11	74.8	78.7	117	BD174675 Ribozyme
12	74.8	78.7	137	BD143601 Method of
13	74.8	78.7	137	BD143079 Sequence
14	74.8	78.7	138	AK153858 Sequence
15	74.8	78.7	141	AK138491 Sequence
16	74.8	78.7	141	BD015659 Slidable
17	74.8	78.7	142	AK138488 Sequence
18	74.8	78.7	142	AK138489 Sequence
19	74.8	78.7	142	AK138490 Sequence

RESULT 1

LOCUS	E33206	DEFINITION	95 bp RNA	LINEAR	PAT	31-JAN-2002
ACCESSION	E33206	Expression system for functional nucleic acid transcription.				
VERSION	E33206.1	GI:18624000				
KEYWORDS	JP 2000059972/A-4.					
SOURCE	synthetic construct					
ORGANISM	synthetic construct					
REFERENCE	other sequences; artificial sequences.					
AUTHORS	Tabira,K., Okawa,A. and Ozeki,S.					
JOURNAL	Expression system for functional nucleic acid transcription					
COMMENT	Patent: JP 2000059972-A 4 07-MAR-2000;					
OS	AGENCY OF IND SCIENCE & TECHNOLOGY					
PN	JP 2000059972/A-4					
PD	07-MAR-2000					
PP	31-AUG-1998	JP 1990244755				
PR						
PI	KAZUNARI TABIRA,ATSUSHI OKAWA,SHIORI OZEKI					
PC	C12N15/09,A61K31/70,A61K35/6,A61K48/00,C12N15/00 CC					
PH						
FT	Location/Qualifiers					
KEY						
FT	Source	1. .95				
FEATURES		/organism='Artificial Sequence'				
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		/mol_type="genomic RNA"				
		/db_xref="taxon:32630"				
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		AX453846 Sequence				
		BD17174 Method for				
		BD174675 Ribozyme				
		BD143601 Method of				
		BD143079 Sequence				
		BD182356 Novel max				
		AK153858 Sequence				
		AK138491 Sequence				
		BD015659 Slidable				
		AK138488 Sequence				
		AK138489 Sequence				

Query Match: 100.0%; Score: 95; DB 6; Length: 95;
 Best Local Similarity: 75.8%; Pred. No. 1.1e-21; Mismatches: 0; Indels: 0; Gaps: 0;

Matches: 72; Conservative: 23; Mismatches: 0; Indels: 0; Gaps: 0;

Origin: 1. ACCTGGAAUUCGUAUAGUACGGGUACGUACGGCAAAACGGCAAAACGGCGGG 60
 1 ACCGTTGGTTGGTAGTGTTGTTCACTTCCTTACACGGCAAAAGTCCCGG 60

Ov Qv 61 UTTGAACCGGCGGAAACAAGAACAGACAUCCGCTU 95
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LOCUS	AX138447	95 bp	RNA
DEFINITION	AX138447.1	GI:14274343	
ACCESSION			
VERSION			
KEYWORD			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Taira, K., Warashina, M., Kuwabara, T. and Kawasaki, H.		
TITLE	Functional ribozyme chimeric molecules capable of sliding		
JOURNAL	Patent: EP 107993-A 8 09-MAY-2001;		
SECRETARY	Secretary of Agency of Industrial Science and Technology (JIP) ;		
TAIRA, Kazunari (JP)			
LOCATION/QUALIFIERS	Location/Qualifiers		
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SOURCE			
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Query Match	100.0%	Score 95; DB 6; Length 95;	
Best Local Similarity	75.8%	Pred. No. 1.1e-21; Mismatches 72; Conservative 23; MisMatches 0; Indels 0; Gaps 0;	
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Qy	1 ACCGGUGGUUCCGUAGUAGUGUUAUCACGUUCGCCUACAGGAAAGGUCCCG	60	
Db	1 AGCTTGATTTCTCGTAGTGTAGTTATCACGTTCGCTAACACGCCAACGTCGG	60	
Qy	61 UTCGAACCGGCGGAAACAAGAACAGACAGUCGUUU	95	
Db	61 TTGAAACCGGGCGGAAACAAGACAGTCGCTT	95	
RESULT	4	AR041184	AR041184
LOCUS	AR041184	132 bp	DNA
DEFINITION	Sequence 17 from patent US 5811275.		
VERSION	AR041184.1	GI:5961680	
KEYWORDS			
ORGANISM			
REFERENCE			
AUTHORS	Wong-Staal, F., Yu, M., Yamada, O., Ojwang, J.O., Leavitt, M. and Ho, A.		
TITLE	HIV-specific ribozymes		
JOURNAL	Patent: US 5811275-A 17 22-SEP-1998;		
FEATURES	Location/Qualifiers		
SOURCE			
ORIGIN			
Query Match	100.0%	Score 95; DB 6; Length 95;	
Best Local Similarity	75.0%	Pred. No. 1.9e-15; Mismatches 18; Conservative 18; MisMatches 2; Indels 0; Gaps 0;	
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Qy	1 ACCGGUGGUUCCGUAGUAGUGUUAUCACGUUCGCCUACAGGAAAGGUCCCG	60	
Db	11 ACCGGTGTCTCGTAGTGTAGTTATCACGTTCGCTAACACGCCAACGTCGG	70	
Qy	61 UTCGAACCGGGCGGAAACAAGAACAGACAGUCGUUU	90	
Db	71 TTGAAACCGGGCGGAAACAAGACAGTCGCTT	90	
RESULT	5	AR113038	AR113038
LOCUS	AR113038	132 bp	DNA
DEFINITION	Sequence 17 from Patent US 6132962.		
VERSION	AR113038	GI:14093360	
KEYWORDS			
ORGANISM			
REFERENCE			
AUTHORS	Ho, A.		
TITLE	Retroviral vectors comprising an anti-hiv or other nucleic acid		
JOURNAL	Patent: US 6132962-A 17 17-OCT-2000;		
FEATURES	Location/Qualifiers		
SOURCE			
ORIGIN			
Query Match	100.0%	Score 95; DB 6; Length 95;	
Best Local Similarity	75.0%	Pred. No. 1.1e-21; Mismatches 72; Conservative 23; MisMatches 0; Indels 0; Gaps 0;	
Matches			
Qy	1 (bases 1 to 132)		
Db	1 Wong-Staal, F., Yu, M., Yamada, O., Ojwang, J.O., Leavitt, M.C. and		
Qy	CC Description of Artificial Sequence: the		
Db	CC nucleotide sequence of		
Qy	CC the transcript of the human placental tRNAval		
Db	CC transcript of the human placental tRNAval		
Qy	Key Location/Qualifiers		

Qy	1 ACCGUGUUGGUUCGGUAGUGUAGUGGUUAUCACCUUCGCCUACACGGAAAGGUCCCGG	/organism="Homo sapiens"
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Qy	61 UUCGAACCGGGGAAACAGAGCA 86	Query Match Best Local Similarity 78.7%; Score 74.8; DB 6; Length 100; Matches 61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;
Db	61 TTCTGAAACCGGGCACTACAACCA 86	DB14675 Ribozyme expression system.
Qy	1 ACCGUGUUGGUUCGGUAGUGUAGUGGUUAUCACCUUCGCCUACACGGAAAGGUCCCGG	Query Match Best Local Similarity 78.7%; Score 74.8; DB 6; Length 100; Matches 61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;
Db	1 ACCGTGGTTCCGTAGTAGTGTATCACCTGCCTAACACGGAAAGGTCCCCGG	DB14675 Ribozyme expression system.
Qy	61 UUCGAACCGGGGAAACAGAGCA 86	Query Match Best Local Similarity 70.9%; Pred. No. 9.5e-15; Indels 0; Gaps 0;
Db	61 TTCTGAAACCGGGCACTACAACCA 86	DB14675 Ribozyme expression system.
RESULT 9		
LOCUS	AX453846	88 bp
DEFINITION	Sequence 5 from Patent EP1213351.	RNA
ACCESSION	AX453846	linear
VERSION	AX453846.1	PAT 06-JUL-2002
KEYWORDS	.	
SOURCE	synthetic construct	
ORGANISM	synthetic construct	
FEATURES	other sequences; artificial sequences.	
REFERENCE	1 Taira, K., Warashina, M. and Warashina, T.	
AUTHORS	Nucleic acid enzymes acquiring an activity for cleaving a target	
TITLE	RNA by recognizing another molecule	
JOURNAL	Patent: EP 1213351-A 5 12-JUN-2002;	
	National Institute of Advanced Industrial Science and Technology	
(JP)	Location/Qualifiers	
source	1. .88 'organism='synthetic construct'" 'mol_type='unassigned RNA'" 'db_xref='taxon:32630'" 'note='tRNA _{val} promoter sequence'"	
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LOCUS	E47174	78.7%; Score 74.8; DB 6; Length 88;
DEFINITION	Best Local Similarity 70.9%; Pred. No. 9.5e-15;	DNA
ACCESSION	E47174	Indels 0; Gaps 0;
VERSION	E47174	Mismatches 61; Conservative 18; Indels 0; Gaps 0;
KEYWORDS		
SOURCE		
ORGANISM	Homo Sapiens (human)	
FEATURES	other sequences; artificial sequences.	
REFERENCE	1 Takebe, Y. and Okawa, J.	
AUTHORS	Ribozyme expression system	
TITLE	Patent: JP 2002262880-A 1 17-SEP-2002;	
JOURNAL	DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,	
OS	YUTAKA TAKEBE, JUN OKAWA	
COMMENT	Artificial Sequence	
	PN JP 2002262880-A/1	
	PD 17-SEP-2002	
	PP 09-MAR-2001 JP 2001067253	
	PI YUTAKA TAKEBE, JUN OKAWA	
	PC C12N5/09, A61K3/71, A61K35/76, A61K48/00, A61P31/18, C12N5/10,	
	PC C12N5/00, C12N5/00, C12N5/10, C12N5/00, C12N5/00	
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	CC tetto-tRNA _{val}	
	PH Key Location/Qualifiers	
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FEATURES	Location/Qualifiers	
REFERENCE	1. .117	
source	'organism='synthetic construct'" 'mol_type='genomic DNA'" 'db_xref='taxon:32630'"	
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LOCUS	E47174	78.7%; Score 74.8; DB 6; Length 117;
DEFINITION	Best Local Similarity 70.9%; Pred. No. 9.5e-15;	DNA
ACCESSION	E47174	Indels 0; Gaps 0;
VERSION	E47174.1	Mismatches 61; Conservative 18; Indels 0; Gaps 0;
KEYWORDS		
SOURCE		
ORGANISM	Homo Sapiens (human)	
FEATURES	other sequences; artificial sequences.	
REFERENCE	1 Takebe, Y. and Okawa, J.	
AUTHORS	Ribozyme expression system	
TITLE	Patent: JP 2002262880-A 1 17-SEP-2002;	
JOURNAL	DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,	
OS	YUTAKA TAKEBE, JUN OKAWA	
COMMENT	Artificial Sequence	
	PN JP 2002262880-A/1	
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	PP 09-MAR-2001 JP 2001067253	
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source	'organism='synthetic construct'" 'mol_type='genomic DNA'" 'db_xref='taxon:32630'"	
ORIGIN		
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DEFINITION	Method of selecting high-function nucleic acid molecule in cell.	RNA
ACCESSION	BD143601	linear
VERSION	BD143601.1	PAT 17-JAN-2003
FEATURES	location/Qualifiers	
source	1. .100	

KEYWORDS	JP 2002125685-A/2.													
SOURCE	synthetic construct													
ORGANISM	synthetic construct													
REFERENCE	other sequences; artificial sequences.													
AUTHORS	Taira, K. and Sano, M.													
TITLE	Method of Selecting high-function nucleic acid molecule in cell													
JOURNAL	Patent: JP 2002125685-A 2 08-MAY-2002;													
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND HIROSHI YATSUHASHI, TECHNOLOGY, KAZUNARI TAIRA	OS Artificial Sequence													
COMMENT	1 (bases 1 to 137)													
PI	KAZUNARI TAIRA, MASAYUKI SANO													
PC	C12N15/09, C12N9/00, C12Q1/02, C12Q1/25, C12Q1/68, C12N15/00 CC													
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PD	08-MAY-2002													
PP	30-OCT-2000 JP 2000331347													
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DEFINITION	Sequence 17 from Patent EP1213351.													
ACCESSION	AX453858													
VERSION	AX453858.1													
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SOURCE	synthetic construct													
ORGANISM	synthetic construct													
REFERENCE	other sequences; artificial sequences.													
AUTHORS	Taira, K., Marashina, M. and Marashina, T.													
TITLE	Nucleic Acid Enzymes acquiring an activity for cleaving a target RNA by recognising another molecule													
JOURNAL	Patent: EP 123351-A 17 12-JUN-2002;													
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VERSION	AX453858.1													
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ORGANISM	synthetic construct													
REFERENCE	other sequences; artificial sequences.													
AUTHORS	Taira, K. and Sano, M.													
TITLE	Method for selecting highly functional nucleic acid molecules within cells													
JOURNAL	Patent: EP 1201751-A 2 02-MAY-2002;													
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AUTHORS	Taira, K., Warabina, M., Kuwahara, T. and Kawasaki, H.													
TITLE	Functional ribozyme chimeric molecules capable of sliding													
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TITLE	Location/Qualifiers													
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AUTHORS	Taira, Kazunari (JP)													
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Query Match	Best Local Similarity 70.9%; Score 74.8; DB 6; Length 141; Matches 61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;				</									

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Search completed: February 18, 2005, 22:02:39
Job time : 1459 secs

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Run on: February 18, 2005, 21:07:17 ; Search time 98 Seconds
 (without alignments)
 1586.187 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: I accguuguguuucceguagu...aaaaacaaagacaguuuu 95

scoring table: IDENTITY_NUC

GappT 10.0 , Gapext 1.0

Searched: 1202784 seqb, 818138359 residues

Total number of hits satisfying chosen parameters: 1367770

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
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 3: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	95.00	0	95.4	US-09-763-520-4
2	79.83	1	133.5	PCT-US94-0500-17
3	76.80	1	132.1	US-08-745-72A-17
4	76.80	1	132.1	US-08-745-433-17
5	76.80	1	132.3	US-08-976-996-17
6	74.77	1	128.4	US-09-63-520-3
7	73.76	1	135.4	US-09-763-520-1
8	73.76	1	141.4	US-09-763-520-2
9	69.87	1	149.4	US-09-63-520-5
10	66.87	1	113.4	US-09-763-520-7
11	66.69	1	110.4	US-09-763-520-6
12	25.26	1	106.4	US-09-63-520-13
13	25.26	1	106.4	US-09-763-520-12
14	23.24	1	109.4	US-09-763-520-12
15	22.42	1	81.4	US-09-355-221-6
16	22.22	1	24.4	US-09-563-724B-71
17	21.88	1	149.4	US-09-513-99C-10149
18	21.82	1	86.1	US-08-447-169R-2112
19	21.22	1	86.4	US-09-360-424-212
20	21.22	1	66.4	US-08-227-76-2
21	22.21	1	64.1	US-09-555-30-10
22	20.42	1	78.4	US-09-270-767-29168
23	20.42	1	93.4	US-09-715-88B-9
24	20.42	1	94.2	US-08-785-750-7
25	20.42	1	94.3	US-09-121-62-1
26	20.42	1	94.3	US-09-205-317-7
27	20.42	1	94.4	US-09-858-728-1

Result No.	Score	Query Match Length	DB ID	Description
28	21.52	1	93.4	US-09-715-88B-9
29	21.52	1	94.2	US-08-785-750-7
30	21.52	1	94.3	US-09-121-62-1
31	21.52	1	94.3	US-09-205-317-7
32	21.52	1	94.4	US-09-858-728-1
33	21.52	1	94.4	US-08-785-750-7
34	21.52	1	94.5	US-09-121-62-1
35	21.52	1	94.5	US-09-205-317-7
36	21.52	1	94.6	US-09-858-728-1
37	21.52	1	94.7	US-08-785-750-7
38	21.52	1	94.7	US-09-121-62-1
39	21.52	1	94.7	US-09-205-317-7
40	21.52	1	94.8	US-09-858-728-1
41	21.52	1	94.8	US-08-785-750-7
42	21.52	1	94.9	US-09-121-62-1
43	21.52	1	94.9	US-09-205-317-7
44	21.52	1	95.0	US-09-858-728-1
45	21.52	1	95.0	US-08-785-750-7

STREET: 201 NORTH FIGUEROA STREET
 CITY: LOS ANGELES
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 90012

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: BERNER, ROBERT
 REGISTRATION NUMBER: 20,121
 REFERENCE/DOCKET NUMBER: PCT/US94/05700

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05700
 FILING DATE: 17 MAY 1994
 CLASSIFICATION:
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Kenneth A.
 REGISTRATION NUMBER: 31,677
 REFERENCE/DOCKET NUMBER: 2307E-567-10

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 213-977-1001
 TELEFAX: 213-977-003

INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 132 base pairs
 STRANDBNESS: single
 TOPOLGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: (96'97)
 OTHER INFORMATION: /note= "insertion location of foreign gene in pol III transcription cassette in vector pMUT"

OTHER INFORMATION: /note= "W = INTERNAL NUCLEOTIDE OTHER INFORMATION: SEQUENCE" US-08-245-742A-17

T 3
 -245-742A-17

QUERIED SEQUENCE: 83.2%; Score 79; DB 5; Length 133;
 LOCAL SIMILARITY: 67.4%; Pred. No. 3,7e-21; Mismatches 10; Indels 0; Gaps 0;

INTERNAL INFORMATION:
 APPLICANT: Wong-Staal, Flossie
 APPLICANT: Yu, Mang
 APPLICANT: Yamada, Osamu
 APPLICANT: Ojwang, Joshua O.
 APPLICANT: Leavitt, Mark
 APPLICANT: Ho, Anthony

TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
 TITLE OF INVENTION: and AIDS
 NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew Tower
 STREET: One Market Plaza, Steuart Street Tower
 CITY: San Francisco
 STATE: California
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,483
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Kenneth A.
 REGISTRATION NUMBER: 31,677
 REFERENCE/DOCKET NUMBER: 2307E-567-10

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-6600
 TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 132 base pairs
 TYPE: nucleic acid
 STRANDBNESS: single
 TOPOLGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: (96'97)
 OTHER INFORMATION: /note= "insertion location of foreign gene in pol III transcription cassette in vector pMUT"

OTHER INFORMATION: /note= "W = INTERNAL NUCLEOTIDE OTHER INFORMATION: SEQUENCE" US-08-245-742A-17

QUERIED SEQUENCE: 80.8%; Score 76.8; DB 1; Length 132;
 BEST LOCAL SIMILARITY: 75.0%; Pred. No. 2,7e-20; Mismatches 18; Indels 0; Gaps 0;

MATCHES: 60; Conservatve 60;

QUERY SEQUENCE: 1 ACGGUGAGUUCGUAGUGUAGUGGUUAUCACCUACGCCAACACGGGAAGGUCCCCGG 60
 DB 11 ACCGTTGGTTCCGTAGTAGTGTTAGCTACGCTCACGGGAACGTCGGCG 70

QUERY SEQUENCE: 61 UTCGAAACGGGGGGAACAGAGATCCWAGGGT 95
 DB 71 TTCGAACACGGGGGAAACA 90

RESULT 4
 US-08-465-483-17
 Sequence 17, Application US/08465483
 Patent No. 5811275

GENERAL INFORMATION:
 APPLICANT: Wong-Staal, Flossie
 APPLICANT: Yu, Mang
 APPLICANT: Yamada, Osamu
 APPLICANT: Ojwang, Joshua O.
 APPLICANT: Leavitt, Mark
 APPLICANT: Ho, Anthony

TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
 TITLE OF INVENTION: and AIDS
 NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew Tower
 STREET: One Market Plaza, Steuart Street Tower
 CITY: San Francisco
 STATE: California
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/062,465
 FILING DATE: 17-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/745,742
 FILING DATE: 17-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Kenneth A.
 REFERENCE/DOCKET NUMBER: 31,677
 REGISTRATION NUMBER: 31,677
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 132 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: (96^97)
 OTHER INFORMATION: /note= "insertion location of foreign gene in pol III transcription cassette in vector pMUT"
 Query Match 80.8%; Score 76.8; DB 1; Length 132;
 Best Local Similarity 75.0%; Pred. No. 2.7e-20;
 Matches 60; Conservative 18; Mismatches 2; Indels 0; Gaps 0;
 OTHER INFORMATION:
 1 ACCGGGAGGTTCCGTAATGTGGTATCACGTTGCCCTACACCGGAACGGTCCCCGG 60
 Qy 61 UUCGAACCGGGGGAAACA 80
 Db 71 TTGAAACCGGGGGAAACA 90

RESULT 5
 US-08-876-996-17
 Sequence 17, Application US/08876996
 Patent No. 6332962
 GENERAL INFORMATION:
 APPLICANT: Wong-Staal, Flossie
 APPLICANT: Yu, Mang
 APPLICANT: Yamada, Osamu
 APPLICANT: Oiwang, Joshua O.
 APPLICANT: Leavitt, Mark
 APPLICANT: Ho, Anthony
 TITLE OF INVENTION: Ribozyme Gene Therapy for HTV Infection
 TITLE OF INVENTION: and AIDS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESS: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Street Tower
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/M-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/876,996
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,742
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Kenneth A.
 REGISTRATION NUMBER: 2307E-567-10
 REFERENCE/DOCKET NUMBER: 2307E-567-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 132 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: (96^97)
 OTHER INFORMATION: /note= "insertion location of foreign gene in pol III transcription cassette in vector pMUT"
 OTHER INFORMATION:
 US-08-876-996-17
 Query Match 80.8%; Score 76.8; DB 3; Length 132;
 Best Local Similarity 75.0%; Pred. No. 2.7e-20;
 Matches 60; Conservative 18; Mismatches 2; Indels 0; Gaps 0;
 OTHER INFORMATION:
 Qy 1 ACCGGGAGGTTCCGTAATGTGGTATCACGTTGCCCTACACCGGAACGGTCCCCGG 60
 Db 11 ACCGTTGGTTCCGTTAGTGAGTGGTATCACGTTGCCCTACACCGGAACGGTCCCCGG 70
 Qy 61 UUCGAACCGGGGGAAACA 80
 Db 71 TTGAAACCGGGGGAAACA 90

RESULT 6
 US-09-763-590-3
 Sequence 3, Application US/09763590
 Patent No. 6740750
 GENERAL INFORMATION:
 APPLICANT: Taira, KAZUNARI
 APPLICANT: OHKAWA, JUN
 APPLICANT: KOSEKI, SHIJI
 TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
 TITLE OF INVENTION: NUCLEIC ACIDS
 FILE REFERENCE: 04853_0059-0000
 CURRENT APPLICATION NUMBER: US/09/763,590
 CURRENT FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: PCT/JP99/04718
 PRIOR FILING DATE: 1999-08-31
 PRIOR APPLICATION NUMBER: JP 10/244755
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 128
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
 US-09-763-590-3
 Query Match 77.9%; Score 74; DB 4; Length 128;
 Best Local Similarity 93.9%; Pred. No. 3.3e-19;
 Matches 77; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ACCGGGAGGTTCCGTAATGTGGTATCACGTTGCCCTACACCGGAACGGTCCCCGG 60
 Db 1 Accggggagggtttccgtatgtggttatcacggttgcctacacggaaacgggtccccgg 60


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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 7
; LENGTH: 113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of an
; Patent No. 6740750
; OTHER INFORMATION: antisense oligonucleotide linker
US-09-763-590-7

Query Match 70.3%; Score 66.8; DB 4; Length 113;
Best Local Similarity 71.4%; Pred. No. 2e-15; 2; Indels 0; Gaps 0;
Matches 50; Conservative 18; Mismatches 1; Gapopen 0;
Qy 1 ACCGUGGUUCCGGAGUGUGGGTAAUCAGUGUACATGCCAAGGUCCCCGG 60
Db 71 ACCGTGTTCCGGTAGTGTTGCTATCGTGCCTAACCGGAAGGTTCCCCGG 12
Oy 61 UUCGAAACCG 70
Db 11 TTGGAGTCG 2

RESULT 11
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIORITY APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIORITY APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 106
; TYPE: DNA
; ORGANISM: Artificial Sequence
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIORITY APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1998-08-31
; PRIORITY APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
; Patent No. 6740750
; OTHER INFORMATION: sense oligonucleotide linker
US-09-763-590-6

Query Match 69.5%; Score 66; DB 4; Length 110;
Best Local Similarity 72.7%; Pred. No. 4.1e-16; 0; Indels 0; Gaps 0;
Matches 48; Conservative 18; Mismatches 0; Gapopen 0;
Qy 1 ACCGUGGUUCCGGAGUGUGGGTAAUCAGUGUACATGCCAAGGUCCCCGG 60
Db 44 ACCGTGTTCCGGTAGTGTTGCTATCGTGCCTAACCGGAAGGTTCCCCGG 103
Oy 61 UUCGAA 66
Db 104 TTGGAA 109

RESULT 12
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIORITY APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIORITY APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 13
; LENGTH: 106
; TYPE: DNA
; ORGANISM: Artificial Sequence
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIORITY APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIORITY APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 122
; TYPE: DNA
; ORGANISM: Artificial Sequence
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIORITY APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIORITY APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 12
; LENGTH: 109
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
; Patent No. 6740750
; OTHER INFORMATION: lower primer including the sequences of R22 and a
; OTHER INFORMATION: terminator
US-09-763-590-12

Query Match 26.3%; Score 25; DB 4; Length 109;
Best Local Similarity 88.0%; Pred. No. 4.2; 0; Indels 0; Gaps 0;
Matches 22; Conservative 3; Mismatches 0; Gapopen 0;
Qy 49 AAGGUCCCCGGUAGAACCGGGC 73
Db 109 AAAGTCCCCGGTCAANACGGGC 85

```

US-09-355-221-6/c
; Sequence 6, Application US/09355221
; Patent No. 6105429
; GENERAL INFORMATION:
; APPLICANT: Barber, Jack
; APPLICANT: Welch, Peter
; APPLICANT: Vei, Soonpin
; APPLICANT: Tritz, Richard
; APPLICANT: Immusol Incorporated

TITLE OF INVENTION: Target-Specific Ribozyme Gene Vector Libraries
FILE REFERENCE: 01655-6-0030018
CURRENT APPLICATION NUMBER: US/09/355,221
CURRENT FILING DATE: 1999-07-23
PRIORITY NUMBER: US 60/037,352
PRIORITY FILING DATE: 1997-01-23
PRIORITY APPLICATION NUMBER: WO PCT/US98/01196
PRIOR FILING DATE: 1998-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 2.1
SEQ ID NO 6
LENGTH: 81

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNA-ribozyme lib

FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(81)
; OTHER INFORMATION: n = g, a, c or t

US-09-355-221-6

Query Match Score 23; DB 4; Length 81;
Best Local Similarity 91.3%; Pred. No. 23;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy	58	CGGUUCGAACCCGGCGGAAACA	80
Db	81	CGGTTCGAAGCCGGGGAAACA	59

RESULT 15

US-09-563-794B-71
; Sequence 71, Application US/09563794B

Patent No. 6808976
; GENERAL INFORMATION:

; APPLICANT: KRUEGER, MARTIN
; APPLICANT: WELCH, PETER J.
; APPLICANT: BARBER, JACK R.
; TITLE OF INVENTION: CELLULAR REGULATORS OF INFECTIOUS AGENTS AND METHODS OF
; TITLE OF INVENTION: USE
FILE REFERENCE: 03916-0801
CURRENT APPLICATION NUMBER: US/09/563,794B
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 71
LENGTH: 24

TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer

US-09-563-794B-71
Query Match Score 22.4; DB 4; Length 24;
Best Local Similarity 70.8%; Pred. No. 26;
Matches 17; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 24 gggttacccatcgctcaacggc 47
Db 1 gggttacccatcgctcaacggc 24

Search completed: February 18, 2005, 22:34:48
Job time : 100 secs

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Om nucleic - nucleic search, using sw model

Run On: February 18, 2005, 21:38:28 ; Search time 253 Seconds

Total number of hits satisfying chosen parameters: 10002998

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listeing first 45 summaries

Result No.	Score	Query Length	DB ID	Description
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2	95	1 accggauugauuccagagu.....aaacaagaacgucuuu	US-10-820-820-4	Sequence 1 acggauugauuccagagu.....aaacaagaacgucuuu 95.
3	95	1 accggauugauuccagagu.....aaacaagaacgucuuu	US-10-820-820-4	Sequence 1 acggauugauuccagagu.....aaacaagaacgucuuu 95.
4	95	1 accggauugauuccagagu.....aaacaagaacgucuuu	US-10-820-820-4	Sequence 1 acggauugauuccagagu.....aaacaagaacgucuuu 95.
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7	95	1 accggauugauuccagagu.....aaacaagaacgucuuu	US-10-820-820-4	Sequence 1 acggauugauuccagagu.....aaacaagaacgucuuu 95.
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9	95	1 accggauugauuccagagu.....aaacaagaacgucuuu	US-10-820-820-4	Sequence 1 acggauugauuccagagu.....aaacaagaacgucuuu 95.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	21.8	22.9	78	US-10-932-182A-166715
2	19.8	77	7	US-10-932-182A-166715
3	19.4	117	6	US-10-932-182A-174531
4	18.2	103	7	US-10-605-923-10887
5	19.2	103	7	US-10-605-923-10887
6	18.9	95	8	US-11-043-312-11
7	18	18.9	117	6 US-10-707-003-1264
8	18	18.9	117	7 US-10-604-984-1264
9	17.8	18.7	100	6 US-10-153-469A-3
10	17.6	18.5	96	6 US-10-932-182A-173417
11	17.6	18.5	104	7 US-10-605-923-13759
12	17.6	18.5	104	7 US-10-605-924-9585
13	17.6	18.5	112	8 US-11-021-016-12
14	17.4	18.3	7	US-10-605-923-17798
15	17.4	18.3	66	7 US-10-605-924-12307
16	17.4	18.3	96	7 US-10-604-945-1471
17	17.4	18.3	96	7 US-10-604-945-1471
18	17.4	18.3	147	6 US-10-932-182A-78301
19	17.2	18.1	25	8 US-11-036-317-439867
20	17.2	18.1	60	6 US-10-605-923-397923
21	17.2	18.1	65	7 US-10-604-945-2007
22	17.2	18.1	65	7 US-10-604-942-36290
23	17.2	18.1	73	6 US-10-708-952A-388244
24	17.2	18.1	82	7 US-10-604-985-809

ALIGNMENTS

RESULT	QY	Db	QY	Db
RESULT 1	8 GUUUCGUAUGUGAGUGGUUAUCAGCUUCACACGGAAAGGUCCCGGUUGAA	73 GCTTCAGTCGTCAGCAGGCGTCAGTCATAATCTGAGGTCGAGTCGAAC	80	14
US-10-932-182A-166715	: : : : : : : : : : : : :	: : : : : : : : : : : : :	: : : : : : : : : : : : :	: : : : : : : : : : : : :
			68 CGCGGCGAACAA	13 CTCCTCGAGCA
			80	1

US-10-932-182A-166715

Organism: *Saccharomyces pastorianus*

Query Match Score 22.9%; DB 6; Length 78;

Best Local Similarity 43.8%; Pred. No. 38; Mismatches 32; Indels 0; Gaps 0;

Matches 32; Conservative 9; Sequence 166715, A

Sequence 174531, A

Sequence 10887, A

Sequence 7522, AP

Sequence 11, APPI

Sequence 1264, AP

Sequence 1264, AP

Sequence 3, APPI

Sequence 17317, A

Sequence 9585, AP

Sequence 12, APPI

Sequence 17798, A

Sequence 12307, A

Sequence 1471, AP

Sequence 65132, A

Sequence 78301, A

Sequence 439867,

Sequence 397923,

Sequence 3007, AP

Sequence 36290, A

Sequence 388244,

Sequence 809, APPI

FILE REFERENCE: 55000

CURRENT APPLICATION NUMBER: US/10/605,923

CURRENT FILING DATE: 2003-11-06

NUMBER OF SEQ ID NOS: 1515668

SOFTWARE: Patentin version 3.2

SEQ ID NO 15457,

RESULT 3
 US-10-932-182A-174531
 ; Sequence 174531, Application US/10932182A
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAO, YOSHIHIRO
 ; APPLICANT: NAKAMURA, NORIHIRO
 ; APPLICANT: KODAMA, YUKIKO
 ; APPLICANT: FUJIMURA, TOMOKO
 ; APPLICANT: ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: 030685-943
 CURRENT APPLICATION NUMBER: US/10/932.182A
 NUMBER OF SEQ ID NOS: 197023
 SEQ ID NO 174531
 CURRENT FILING DATE: 2004-09-02
 LENGTH: 117
 ; TYPE: DNA
 ; ORGANISM: *Saccharomyces pastorianus*
 US-10-932-182A-174531

Query Match 19.8%; Score 18.8; DB 7; Length 77;
 Best Local Similarity 45.7%; Pred. No. 5.1e+02;
 Matches 21; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 16 AGUGUAGUGGUUAUCAGGUUCGCUAACACGCCAAAGGUCCGGU 61
 Db 47 AGGTTGCATTAACCTTGCTCAGAGCCAAAGCTCTCATGT 2

RESULT 4
 US-10-605-923-1087
 ; Sequence 10887, Application US/10605923
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSETTA GENOMICS LTD
 ; TITLE OF INVENTION: BIINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: 55000
 ; CURRENT APPLICATION NUMBER: US/10/605, 923
 CURRENT FILING DATE: 2003-11-06
 NUMBER OF SEQ ID NOS: 1515668
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 10887
 LENGTH: 103
 ; TYPE: DNA
 ; ORGANISM: *Homo Sapiens*
 US-10-605-923-1087

Query Match 19.4%; Score 18.4; DB 6; Length 117;
 Best Local Similarity 56.8%; Pred. No. 7.8e+02;
 Matches 25; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

Qy 30 CAGGUCCACACCGCAAGGUCCGGU 73
 Db 54 CAGGTATGCAAGCATGGAAGGCCCTGGTCAATTCCAGC 97

RESULT 5
 US-10-605-923-1087
 ; Sequence 10887, Application US/10605923
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSETTA GENOMICS LTD
 ; TITLE OF INVENTION: BIINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: 55000
 ; CURRENT APPLICATION NUMBER: US/10/605, 923
 CURRENT FILING DATE: 2003-11-06
 NUMBER OF SEQ ID NOS: 1515668
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 10887
 LENGTH: 103
 ; TYPE: DNA
 ; ORGANISM: *Homo Sapiens*
 US-10-605-923-1087

Query Match 19.2%; Score 18.2; DB 7; Length 103;
 Best Local Similarity 44.7%; Pred. No. 9e+02;
 Matches 21; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 8 GUUCCGAGGUGUAGGUUAUCAGGUUCGCUAACACGCCAAAGGU 54
 Db 21 GATTCGGACTGAAATGGTATGAGTAAAGCCATAGGT 67

RESULT 6
 US-11-043-312-11
 ; Sequence 11, Application US/11043312
 ; GENERAL INFORMATION:
 ; APPLICANT: COLOSI, PETER C.
 TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
 NUMBER OF SEQID NOS: 17
 CURRENT FILING DATE: 2003-09-11
 ; RECOMBINANT AAV VIRION PRODUCTION
 CORRESPONDENCE ADDRESS:
 ADDRESS: REED & ROBINS LLP
 STREET: 285 HAMILTON AVENUE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/11/043,312
 FILING DATE: 26-Jan-2005
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10/177,871
 FILING DATE: 19-Jun-2002
 APPLICATION NUMBER: US/08/745,957
 FILING DATE: 07-Nov-1996
 APPLICATION NUMBER: US 60/006,402
 FILING DATE: 09-Nov-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: McCracken, Thomas P.
 REGISTRATION NUMBER: 38,548
 REFERENCE/DOCKET NUMBER: 0800-0007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 327-3400
 TELEFAX: (415) 327-3231
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 95 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-11-043-312-11

RESULT 5
 US-10-605-924-7522
 ; Sequence 7522, Application US/10605924
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSETTA GENOMICS LTD
 ; TITLE OF INVENTION: BIINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
 ; TITLE OF INVENTION: USES THEREOF
 FILE REFERENCE: 55004
 CURRENT APPLICATION NUMBER: US/10/605, 924
 CURRENT FILING DATE: 2003-11-06
 NUMBER OF SEQ ID NOS: 1388402
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 7522
 ; TYPE: DNA
 ; ORGANISM: *Homo Sapiens*
 US-10-605-924-7522

Query Match 19.2%; Score 18.2; DB 7; Length 103;
 Best Local Similarity 44.7%; Pred. No. 9e+02;
 Matches 21; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 8 GUUCCGAGGUGUAGGUUAUCAGGUUCGCUAACACGCCAAAGGU 54
 Db 21 GATTCGGACTGAAATGGTATGAGTAAAGCCATAGGT 67

Query Match ; 18.9%; Score 18; DB 8; Length 95;
Best Local Similarity 69.2%; Pred. No. 1.1e+03; Mismatches 5; Indels 0; Gaps 0;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 43 CACGCGAAAGGUCCCCGGUCCRAAC 68
Db 8 CACGCGTGAGTCCGGGTTCTGAGC 33

RESULT 7 ; Sequence 3, Application US/10153469A
US-10-707-003-1264 ; GENERAL INFORMATION:
; SEQUENCE 1264, Application US/10107003
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOMINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
FILE REFERENCE: 55030
CURRENT APPLICATION NUMBER: US/10/707, 003
CURRENT FILING DATE: 2003-10-30
NUMBER OF SEQ ID NOS: 46755
SOFTWARE: Patentin version 3.2
SEQ ID NO 1264
LENGTH: 117
TYPE: DNA
ORGANISM: Human enterovirus C
US-10-707-003-1264

Query Match ; 18.9%; Score 18; DB 6; Length 117;
Best Local Similarity 39.2%; Pred. No. 1.1e+03; Mismatches 35; Indels 0; Gaps 0;
Matches 29; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

QY 16 ACUGUACUGGUUAUCAGGUUCCCUAACACGGAAAGGUCCCCGGUUCGAACCGGGGG 75
Db 7 AGTGTATAATTAGATTACCCACATGGTGTACTCTGCTGTTGAGAACGAGG 66

QY 76 AACAAAGAGACUC 89
Db 67 TGATAAAGATAGAC 80

RESULT 8 ; Sequence 3, Application US/10153469A
US-10-604-984-1264 ; GENERAL INFORMATION:
; SEQUENCE 154, Application US/101064984
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOMINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
FILE REFERENCE: 55010
CURRENT APPLICATION NUMBER: US/10/604, 984
CURRENT FILING DATE: 2003-08-29
NUMBER OF SEQ ID NOS: 46755
SOFTWARE: Patentin version 3.2
SEQ ID NO 1264
LENGTH: 117
TYPE: DNA
ORGANISM: Human enterovirus C
US-10-604-984-1264

Query Match ; 18.9%; Score 18; DB 7; Length 117;
Best Local Similarity 39.2%; Pred. No. 1.1e+03; Mismatches 35; Indels 0; Gaps 0;
Matches 29; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

QY 16 ACUGUACUGGUUAUCAGGUUCCCUAACACGGAAAGGUCCCCGGUUCGAACCGGGGG 75
Db 7 AGTGTATAATTAGATTACCCACATGGTGTACTCTGCTGTTGAGAACGAGG 66

RESULT 9 ; Sequence 3, Application US/10153469A
US-10-707-003-1264 ; GENERAL INFORMATION:
; SEQUENCE 1264, Application US/10107003
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOT A.
; BUECHTER, DOUGLAS
; BROKAW, JANE
; PROBLELLA, DAVID
; ZHANG, GUANGHUI
; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
; NUMBER OF SEQUENCES: 50
; NUMBER OF SEQ ID NOS: 46755
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1264
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Human enterovirus C
US-10-707-003-1264

Query Match ; 18.9%; Score 18; DB 6; Length 117;
Best Local Similarity 39.2%; Pred. No. 1.1e+03; Mismatches 35; Indels 0; Gaps 0;
Matches 29; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

QY 16 ACUGUACUGGUUAUCAGGUUCCCUAACACGGAAAGGUCCCCGGUUCGAACCGGGGG 75
Db 7 AGTGTATAATTAGATTACCCACATGGTGTACTCTGCTGTTGAGAACGAGG 66

QY 76 AACAAAGAGACUC 89
Db 67 TGATAAAGATAGAC 80

RESULT 10 ; Sequence 3, Application US/10153469A
US-10-153-469A-3 ; GENERAL INFORMATION:
; SEQUENCE 173417, Application US/101032182A
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIIRO
; APPLICANT: NAKAMURA, NORIHSA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 0310685-043
CURRENT APPLICATION NUMBER: US/10/932.182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 173417
LENGTH: 96
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-173417

RESULT 9 ; Sequence 3, Application US/10153469A
US-10-153-469A-3

; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-05
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 12307
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-605-924-12307

Query Match 18.3%; Score 17.4; DB 7; Length 66;
Best Local Similarity 47.5%; Pred. No. 1.6e+03;
Matches 28; Conservative 5; Mismatches 26; Indels 0; Gaps 0;
Qy 12 CCGUAGUGAGUGGUUAUCAGGUCCUAACAGGGAAGGUCCCCGGGUUCGAAACCG 70
Db 65 CTGACCTGGAAACCATCATCACCGAACCGAGGGGGAGGTGGTGAATGGAACCG 7

Search completed: February 18, 2005, 23:20:04
Job time : 256 SECs

GenCore version 5.1.6
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On nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:00:02 ; Search time 1819 Seconds
 (without alignments)
 1987.963 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: 1 accguuguuuucggauagu.....aaacaaagacagucuuu 95

Scoring table: IDENTITY_NUC

Gapop 10-0 , Gapext 1.0

Searched: 34239544 seqs, 19012134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST+*

1: gb_elt1:+

2: gb_elt2:+

3: gb_hoc:+

4: gb_elt3:+

5: gb_elt4:+

6: gb_elt5:+

7: gb_elt6:+

8: gb_elt8:+

9: gb_gel8:+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	40.4	42.5	57 2	BB031637
2	31.5	32.6	150 5	B0277850 Cr_Emb_08
3	30.2	31.8	71 9	BX203515
4	30.1	31.6	135 6	CB495943
5	29.2	30.7	130 4	BB845249
6	29.2	30.7	147 9	AL763279
7	28.2	29.7	124 9	DR366G28
8	26.6	28.0	136 8	A2927512
9	26.4	27.8	137 6	BZ395589
10	26.4	27.8	144 9	BX166029
11	25.8	27.2	149 9	DR21E138
12	25.6	26.9	126 7	HO4713
13	25.2	26.5	109 6	CD768762
14	25.2	26.5	112 6	CD769207
15	24.8	26.1	37 9	AL757571
16	24.8	26.1	134 9	BX126117
17	24.6	25.9	122 5	BB203653
18	24.4	25.7	121 5	A1013006
19	24.2	25.5	64 2	BF118530
20	24.2	25.5	126 9	BK247709
c	21	24.2	103 1	AU259857
c	22	24	25.3	BX233421
c	23	24	25.3	AU758558
c	24	24	122 9	Danio rer
25	25.3	123 9	BX148475	

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On nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:00:02 ; Search time 1819 Seconds
 (without alignments)
 1987.963 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: 1 accguuguuuucggauagu.....aaacaaagacagucuuu 95

Scoring table: IDENTITY_NUC

Gapop 10-0 , Gapext 1.0

Searched: 34239544 seqs, 19012134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST+*

1: gb_elt1:+

2: gb_elt2:+

3: gb_hoc:+

4: gb_elt3:+

5: gb_elt4:+

6: gb_elt5:+

7: gb_elt6:+

8: gb_elt8:+

9: gb_gel8:+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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On nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:00:02 ; Search time 1819 Seconds
 (without alignments)
 1987.963 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: 1 accguuguuuucggauagu.....aaacaaagacagucuuu 95

Scoring table: IDENTITY_NUC

Gapop 10-0 , Gapext 1.0

Searched: 34239544 seqs, 19012134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST+*

1: gb_elt1:+

2: gb_elt2:+

3: gb_hoc:+

4: gb_elt3:+

5: gb_elt4:+

6: gb_elt5:+

7: gb_elt6:+

8: gb_elt8:+

9: gb_gel8:+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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On nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:00:02 ; Search time 1819 Seconds
 (without alignments)
 1987.963 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: 1 accguuguuuucggauagu.....aaacaaagacagucuuu 95

Scoring table: IDENTITY_NUC

Gapop 10-0 , Gapext 1.0

Searched: 34239544 seqs, 19012134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST+*

1: gb_elt1:+

2: gb_elt2:+

3: gb_hoc:+

4: gb_elt3:+

5: gb_elt4:+

6: gb_elt5:+

7: gb_elt6:+

8: gb_elt8:+

9: gb_gel8:+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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On nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:00:02 ; Search time 1819 Seconds
 (without alignments)
 1987.963 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: 1 accguuguuuucggauagu.....aaacaaagacagucuuu 95

Scoring table: IDENTITY_NUC

Gapop 10-0 , Gapext 1.0

Searched: 34239544 seqs, 19012134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST+*

1: gb_elt1:+

2: gb_elt2:+

3: gb_hoc:+

4: gb_elt3:+

5: gb_elt4:+

6: gb_elt5:+

7: gb_elt6:+

8: gb_elt8:+

9: gb_gel8:+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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On nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:00:02 ; Search time 1819 Seconds
 (without alignments)
 1987.963 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: 1 accguuguuuucggauagu.....aaacaaagacagucuuu 95

Scoring table: IDENTITY_NUC

Gapop 10-0 , Gapext 1.0

Searched: 34239544 seqs, 19012134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST+*

1: gb_elt1:+

2: gb_elt2:+

3: gb_hoc:+

4: gb_elt3:+

5: gb_elt4:+

6: gb_elt5:+

7: gb_elt6:+

8: gb_elt8:+

9: gb_gel8:+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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On nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:00:02 ; Search time 1819 Seconds
 (without alignments)
 1987.963 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: 1 accguuguuuucggauagu.....aaacaaagacagucuuu 95

Scoring table: IDENTITY_NUC

Gapop 10-0 , Gapext 1.0

Searched: 34239544 seqs, 19012134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST+*

1: gb_elt1:+

2: gb_elt2:+

3: gb_hoc:+

4: gb_elt3:+

5: gb_elt4:+

6: gb_elt5:+

7: gb_elt6:+

8: gb_elt8:+

9: gb_gel8:+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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On nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:00:02 ; Search time 1819 Seconds
 (without alignments)
 1987.963 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: 1 accguuguuuucggauagu.....aaacaaagacagucuuu 95

Scoring table: IDENTITY_NUC

Gapop 10-0 , Gapext 1.0

Searched: 34239544 seqs, 19012134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST+*

1: gb_elt1:+

2: gb_elt2:+

3: gb_hoc:+

4: gb_elt3:+

5: gb_elt4:+

6: gb_elt5:+

7: gb_elt6:+

8: gb_elt8:+

9: gb_gel8:+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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On nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:00:02 ; Search time 1819 Seconds
 (without alignments)
 1987.963 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: 1 accguuguuuucggauagu.....aaacaaagacagucuuu 95

Scoring table: IDENTITY_NUC

Gapop 10-0 , Gapext 1.0

Searched: 34239544 seqs, 19012134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0

Maximum DB seq length: 150

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST+*

1: gb_elt1:+

2: gb_elt2:+

3: gb_hoc:+

4: gb_elt3:+</

ORIGIN

Query Match 42.5%; Score 40.4; DB 2; Length 57;
 Best Local Similarity 66.0%; Pred. No. 0.0026; Mismatches 33; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Matched 39; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 18 USUAGUGGUUAUCAGGUCCUAACGGGAAGGUCCCCGGUCAA 67
Db 1 TCTTAGCGTTATCACATTCGCTCAGCGGAAGGTCCTTATAA 50

RESULT 2
LOCUS BU275850 150 bp mRNA linear EST 03-JAN-2003
DEFINITION Cr_Emb_08F08_TEXP1 Convoluta roscoffensis embryos from Eva Jimenez sequence.
ACCESSION BU275850
VERSION BU275850.1
KEYWORDS EST, Symbagittifera roscoffensis

ORGANISM Symbagittifera roscoffensis
 Eukaryota; Metazoa; Plathelminthes; Turbellaria; Acoelomorpha; Acoela; Sagittiferidae; Symbagittifera.
 1 (bases 1 to 150)
AUTHORS Blaxter,M.L., Jiminez,E., Rosse,A., Aboobaker,A. and Salo,E.

TITLE A survey of genes expressed in the acoel flatworm Convoluta roscoffensis
 Unpublished (2002)

COMMENT Contact: Blaxter ML
 Institute of Cell, Animal and Population Biology
 University of Edinburgh
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JT, UK.
 Tel: +44 131 650 6760
 Fax: +44 131 670 5450
 Email: mark.blaxter@ed.ac.uk
 The library was prepared by Eva Jimenez, University of Barcelona, Spain. The sequencing was performed by Eva Jimenez, Aziz Aboobaker and Ailie Rosie, Edinburgh Phlogenomics Programme, ICAPB, Edinburgh, UK. The sequence contained a Polya tail (trimmed)

PCR PRIMERS
FORWARD: T7PFL
BACKWARD: triple 5 ExSeq
Plate: 08 **row:** F **column:** 08
Seg primer: TEXP1
 High quality sequence stop: 150.

FEATURES
source

1. 150 Location/Qualifiers

/organism="Symbagittifera roscoffensis"
/mol_type="mRNA"
/db_xref="raxon_84072"
/clone="Cr_Emb_08F08"
/sex="mixed"
/dev_stage="embryo"
/clone_lib="Convoluta roscoffensis embryos from Eva Jiminez"
/notes="Vector: lambda triplex; Site 1: SCDRI; Site_2: HindIII; The library was prepared by Eva Jimenez, University of Barcelona, Spain. The sequencing was performed by Eva Jimenez, Aziz Aboobaker and Ailie Rosie, Edinburgh Phylogenomics Programme, ICAPB, Edinburgh, UK."
ORIGIN

ORIGIN

Query Match 31.8%; Score 30.2; DB 9; Length 71;
 Best Local Similarity 49.3%; Pred. No. 1.9; Mismatches 33; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

Matched 39; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 9 UUUCGGAGGUGUGUGUUAUCAGGUCCUAACGGGAAGGUCCCCGGUCAA 68
Db 2 TTGGAGTGCTCATGTGTTAGCTACCCTGCCCTCACAGTAANAGGTACTGGTTAAC 61

RESULT 4
LOCUS CB495943 135 bp mRNA linear EST 27-MAR-2003
DEFINITION Oncorhynchus mykiss CDNA, mRNA sequence.
ACCESSION CB495943
VERSION CB495943.1
KEYWORDS EST,
ORGANISM Oncorhynchus mykiss (rainbow trout)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 135)
AUTHORS GRASP Consortium, Davidson,W.S., Koop,B.P. and http://web.uvic.ca/cb/grasp.
 A survey of *Salmo salar* transcripts from high complexity cDNA libraries
 Unpublished (2002)
COMMENT Contact: Koop BP
 Centre for Biomedical Research
 PO Box 3020 SNN CSC, Victoria BC, V8W 3N5, Canada
 Tel: 250 472 4067

QY 7 GGUUUCGGUGUGUGUUAUCAGGUCCUAACGGGAAGGUCCCCGGUCAA 66
Db 26 GGAGCAGTGAGTGAGTGTGCTCCGCCTCAATGAAAGGTGATGTTCAAG 85
QY 67 ACCGGCGGAAACAAAGACGUCCU 93

Pax: 250 472 4075
 Email: bkoopewovic.ca
 Centre for Biomedical Research, University of Victoria cDNA
 preparation and sequencing: Roberto Alberto, Marianne
 Bettz-Sargent, Maura Babby, Peter Hunt, Linda McInnes, BF Koop.
 biInformatics: Gordon D Brown.
 Location/Qualifiers

FEATURES

source 1. 135

/organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="Chilliwack River steelhead"
 /clone_lib="Oncorhynchus mykiss Chilliwack River Steelhead whole"
 /note="Vector: pBlueScriptTKS+; Library Creator: Matthew L Rose, BF Koop ; Rainbow trout tissue contributors: Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN

Query Match 31.6%; Score 30; DB 6; Length 135;
 Best Local Similarity 48.6%; Pred. No. 2,5; Matches 34; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

Matches 34; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

Qy 14 GUGAGUGAGUGAGGUAACGUGGCCUACGGGAAGGGCCGCGGUACGGGC 73
 65 GTGCGCTAGTCGTAGAGCGTTGACTGTAACCGGAGGTGCGACTCAACCCGA 124

Db 74 GGAACAAAG 83

Db 125 GGTGACAGG 134

RESULT 5

B1845249/c LOCUS BI145249 130 bp mRNA linear EST 04-OCT-2001 DEFINITION f82a07.y1 Zebrafish neuronal Danio rerio clone IMAGB:5077140 ACCESSION B1845249 VERSION 1.0 AUTHOR EST. SOURCE

ORGANISM Danio rerio (zebrafish)

DEFINITION f82a07.y1 Zebrafish neuronal Danio rerio clone IMAGB:5077140 5' mRNA sequence.

ACCESSION B1845249.1 VERSION 1.0 AUTHOR EST. SOURCE

ORGANISM Danio rerio (zebrafish)

DEFINITION f82a07.y1 Zebrafish neuronal Danio rerio clone IMAGB:5077140 5' mRNA sequence.

ACCESSION B1845249.1 VERSION 1.0 AUTHOR EST. SOURCE

ORGANISM Danio rerio (zebrafish)

DEFINITION f82a07.y1 Zebrafish neuronal Danio rerio clone IMAGB:5077140 5' mRNA sequence.

ACCESSION B1845249.1 VERSION 1.0 AUTHOR EST. SOURCE

ORGANISM Danio rerio (zebrafish)

REFERENCE

AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.

TITLE GABI-Kat SimpleSearch: a Flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in *Arabidopsis thaliana*

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829
 PUBMED 12874060

REFERENCE

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

TITLE An *Arabidopsis thaliana* T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE 23117147
 PUBMED 14756321

REFERENCE

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized *Arabidopsis thaliana* lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

MEDLINE 1462050
 PUBMED 14756321

REFERENCE

AUTHORS Rosso, M.G., Li, Y., Strizhov, N. and Weisshaar, B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50209, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g05830. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpi-z-koeln.mpg.de/GABI-kat/>.

FEATURES

source 1. .130

/organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="Taxon:7955"
 /clone="IMAGE:5077140"
 /bbox="mixed"
 /dev_stage="adult"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"

ORIGIN

Query Match 30.7%; Score 29.2; DB 4; Length 130;
 Best Local Similarity 53.4%; Pred. No. 5; Matches 31; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Matches 31; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Qy 8 GTCGGCGGAGGGTGGTAGCAGCTACAGGAGATCACTGGTCA 65
 Db 63 GTCAGGGCGCAGTGGTAGCAGCTACAGGAGATCACTGGTCA 6

RESULT 6

AL763279/c LOCUS AL763279 147 bp DNA linear GSS 01-APR-2004 DEFINITION *Arabidopsis thaliana* T-DNA flanking sequence GK-035E01-015008, genomic survey sequence.

ACCESSION AL763279 VERSION AL763279.1 GI:215212136

KEYWORDS GSS.

SOURCE *Arabidopsis thaliana* (thale cress)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1. Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.

AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.

TITLE GABI-Kat SimpleSearch: a Flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in *Arabidopsis thaliana*

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829
 PUBMED 12874060

REFERENCE

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

TITLE An *Arabidopsis thaliana* T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE 23117147
 PUBMED 14756321

REFERENCE

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized *Arabidopsis thaliana* lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

MEDLINE 1462050
 PUBMED 14756321

REFERENCE

AUTHORS Rosso, M.G., Li, Y., Strizhov, N. and Weisshaar, B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50209, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g05830. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpi-z-koeln.mpg.de/GABI-kat/>.

FEATURES

source 1. .147

/organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="Taxon:3702"
 /clone="GK-035E01-015008"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"
 /notes="PCR was performed on DNA from *Arabidopsis thaliana*
 plants (T1) which were transformed with the T-DNA from
 vector PAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

ORIGIN

Query Match
 Best Local Similarity 53.4%; Pred. No. 5.2;
 Matches 31; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
 Oy 23 TGCATGACGAGGCGCCAAACGGGAAGGUCCCCGCGTAA 80
 Db 94 TGCTTAGAGCGGTGTCATGAGCGAGTGCGGAGTTGAGCCGCGAAGCA 37

RESULT 7

DR36G28/c DR36G28 124 bp DNA linear GSS 22-NOV-2002
 DEFINITION Danio rerio genomic clone DKEY-36G2, genomic survey sequence.
 ACCESSION AL985516
 VERSION AL985516.1 GI:25180237
 KEYWORDS GSS
 SOURCE
 ORGANISM

Danio rerio (zebrafish)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 124)
 Humpfrey,S.J., Huckle, E. and Hunt,S.E.

TITLE Direct Submission
 JOURNAL Submitted [14-NOV-2002] The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
 humquery@sanger.ac.uk Unpublished part of the BAC Library created by R. Plasterk and N.V.
 Kyogen. This sequence was generated from the SP6 end of BAC 36G2. 36G2 is
 part of the Daniokey BAC Library created by R. Plasterk and N.V.
 Further detail: http://www.sanger.ac.uk/Projects/D_rerio/.

COMMENT
 FEATURES source
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

1. .124
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="Taxon:7955"
 /clone="DKEY-36G2"
 /tissue_type="testis"
 /notes="vector pindigOBAC-536"

ORIGIN

Query Match
 Best Local Similarity 49.3%; Pred. No. 12;
 Matches 36; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

Oy 8 GUUUCGUGUAGGUGUAAAUCAGGUCCGCUAACACGGGAAGGUCCCCGCGTAA 67
 Db 97 GTGCACTAATGGCTCAGTGGTACATGATGCTCACACAGAGGTCACTGGTGGC 38

Oy 68 CCGGGGAAACA 80
 Db 37 CCTGGCTGGTCA 25

RESULT 8

A2927512/c A2927512 136 bp DNA linear GSS 01-APR-2001
 DEFINITION 47.6-dit25fil.81 Saccharomyces castellii NRL Y-12630 Naumovia
 accession A2927512
 version A2927512.1 GI:13499416
 keywords GSS
 source Naumovia castellii

ORGANISM

Naumovia castellii

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Naumovia.

1 (bases 1 to 136)

Clinten,P.F., Waterston,R.H. and Johnston,M.

Gish,W.R., Surveying Saccharomyces genomes to identify functional elements by

comparative DNA sequence analysis

Unpublished (2001)

Contact: Johnston,M

Department of Genetics

Washington University Medical School

Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA

Tel: 314 362 2735

Fax: 314 362 7855

Email: mjl@genetics.wustl.edu

Class: random plasmid subclone.

Location/Qualifiers

1. .136

/organism="Naumovia castellii"

/mol_type="genomic DNA"

/strain="NRRL Y-12630 (CBS 4309)"

/db_xref=Taxon:27288

/clone="47.6-dit25fil.81"

/clone_id="Saccharomyces castellii NRRL Y-12630"

/note="Random genomic sequence"

ORIGIN

Query Match
 Best Local Similarity 68.3%; Pred. No. 49;
 Matches 28; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

RESULT 9
 BZ396589 BZ396589 BI_10_12_kb Entamoeba invadens genomic clone BINAN55,
 DEFINITION BZ396589
 ACCESSION BZ396589
 VERSION 1
 KEYWORDS GSS
 SOURCE
 ORGANISM

Entamoeba invadens
 Eukaryota; Entamoebidae; Entamoeba.
 1 (bases 1 to 137)

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Other_GSSB: BINAN55TR

Contact: Brendan Loftus

Department of Entamoebic Genomics

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: enta@tigr.org

DNA was provided by Daniel Eichinger

Sq. Primer: TP

Class: Sheared ends.

Location/Qualifiers

1. .137

/organism="Entamoeba invadens"

/mol_type="genomic DNA"

/strain="P-1"

/db_xref=Taxon:33085

/clone="BINAN55"

Best Local Similarity 50.0%; Pred. No. 1.1e+02; Mismatches 29; Indels 0; Gaps 0;

Matched 36; Conservative 7; Mismatches 29; Indels 0; Gaps 0;

OY 15 uacugucagcgguaacacggaaaggcccaatcacggggggaaacaaaa 74

Db 51 TACTCAGTGTAGGGCTTCGCTAGGAAGCAGGCCCTGGTTGGTCCCAGCT 110

OY 75 GAACAAAGCA 86

Db 111 CTGAAAGA 122

RESULT 13

CD768762 CD768762 109 bp mRNA linear EST 02-JUL-2003

LOCUS AGENCOURT 14715419 NICHD MM_Hyp1 Mus musculus cDNA clone IMAGE:6975|075', mRNA sequence.

ACCESSION CD768762

VERSION CD768762.1

KEYWORDS EST.

SOURCE

ORGANISM Mus musculus (house mouse)

REFERENCE NIH-MGC http://mgc.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Daniela S. Gerhard, Ph.D.

COMMENT

Office of Cancer Genomics

National Cancer Institute / NIH

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 109)

1 (bases 1 to 112)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabbs@mail.nih.gov

Tissue Procurement: Dr. Pamela Mellon and Dr. Pat Chappell

cDNA Library Preparation: Clontech Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LInN)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LInN at:

<http://image.llnl.gov>

Plate: LINC3275 row: C column: 10

High quality sequence stop: 109;

Locality/Qualifiers

FEATURES

Source

1. .109

/organism="Mus musculus"

/mol_type="mRNA"

/ab_xref="txon:10090"

/lab_host="DH10B (phage-resistant)"

/clone="IMAGE:6975107"

/lab_host="DH10B (phage-resistant)"

/clone="NICHD MM_Hyp1"

/notes="Organ: brain - normal mediobasal hypothalamus; Vector: pDNR-LIB; Site 1: SfiI (ggccatttggcc); Site 2: SfiI (ggccgttcggcc); Non-normalized full-length enriched library 5' and 3'; adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3', and 3' adaptor sequence: 5'-ATTCAGAGCGGAGGGGAGATG-3'(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.08 kb (range .73-1.37 kb). 13/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Corp."

ORIGIN

Query Match 26.5%; Score 25.2; DB 6; Length 112;

Best Local Similarity 54.8%; Pred. No. 1.6e+02; Mismatches 34; Conservative 5; Indels 0; Gaps 0;

OY 25 GUUUCACGGUGCCUAACCGGAAAGGCGGAAACGGGGGGAAACAAA 84

Db 26 GGTTAGCGCTTGCTTAGGAGCGSCAGGCGCTGGTCTCAGAAAAA 85

RESULT 15

AL757571 AL757571

LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-150B02-013073,

DEFINITION

Best Local Similarity 50.0%; Pred. No. 1.1e+02; Mismatches 29; Indels 0; Gaps 0;

Matched 36; Conservative 7; Mismatches 29; Indels 0; Gaps 0;

OY 15 uacugucagcgguaacacggaaaggcccaatcacggggggaaacaaaa 74

Db 51 TACTCAGTGTAGGGCTTCGCTAGGAAGCAGGCCCTGGTTGGTCCCAGCT 110

RESULT 14

CD769207 CD769207 112 bp mRNA linear EST 02-JUL-2003

LOCUS AGENCOURT 14720166 NICHD MM_Hyp1 Mus musculus cDNA clone IMAGE:6974510 5', mRNA sequence.

ACCESSION CD769207

VERSION CD769207.1

KEYWORDS EST.

SOURCE

ORGANISM Mus musculus (house mouse)

REFERENCE NIH-MGC http://mgc.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Daniela S. Gerhard, Ph.D.

COMMENT

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabbs@mail.nih.gov

Tissue Procurement: Dr. Pamela Mellon and Dr. Pat Chappell

cDNA Library Preparation: Clontech Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LInN)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LInN at:

<http://image.llnl.gov>

Plate: LINC3273 row: J column: 13

High quality sequence stop: 112;

Locality/Qualifiers

FEATURES

Source

1. .112

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:6974510"

/lab_host="DH10B (phage-resistant)"

/clone="DH10B (phage-resistant)"

/notes="Organ: brain - normal mediobasal hypothalamus; Vector: pDNR-LIB; Site 1: SfiI (ggccatttggcc); Site 2: SfiI (ggccgttcggcc); Non-normalized full-length enriched library 5' and 3'; adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCAGAGCGGAGGGGAGATG-3'(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.08 kb (range .73-1.37 kb). 13/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Corp."

ORIGIN

Query Match 26.5%; Score 25.2; DB 6; Length 112;

Best Local Similarity 54.8%; Pred. No. 1.6e+02; Mismatches 34; Conservative 5; Indels 0; Gaps 0;

OY 25 GUUUCACGGUGCCUAACCGGAAAGGCGGAAACGGGGGGAAACAAA 84

Db 26 GGTTAGCGCTTGCTTAGGAGCGSCAGGCGCTGGTCTCAGAAAAA 85

RESULT 15

AL757571 AL757571

LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-150B02-013073,

DEFINITION

Job time : 1827 secs

Genomic survey sequence.

ACCESSION AL375751
 VERSION 1
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots;
 roids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.
 TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 MEDLINE 22155829
 PUBMED 12274060
 REFERENCE 2
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 Weisshaar, B.
 TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 Flanking Sequence tag-based reverse genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 MEDLINE 23117147
 PUBMED 14956321
 REFERENCE 3
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
 Weisshaar, B.
 TITLE High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
 PUBMED 14682050
 REFERENCE 4 (bases 1 to 37)
 AUTHORS Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.
 TITLE Direct Submission
 Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion close to or within gene Atg50840.
 Details on the protocols used for generation of the sequence are
 described in References 1-3. The sequences are generated at the MPI
 for Plant Breeding Research in the context of the GABI-Kat project.
 GABI-Kat is part of the German Plant Genomics program designated
 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES Location/Qualifiers

source 1. 37

/organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strains="Columbia 0"
 /db_xref="taxon:3702"
 /clone=GK-150502-013073"
 /clone_id="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161 (GenBank accession number: AJ337514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

ORIGIN

Query Match 26.1%; Score 24.8; DB 9; Length 37;
 Best Local Similarity 66.7%; Pped. No. 1.8e+02;
 Matches 24; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy	28	AUCACGUUCGCCAACAGCGGAAGGUCCCGAUC	63
Db	2	ATCACGTTGCTTACACGGAAAGGCTCGGTC	37

GenCore version 5.1.6
copyright (c) 1993 - 2005 Compugen Ltd.

On nucleic - nucleic search, using sw model

Run on: February 18, 2005, 22:02:48 ; Search time 313 Seconds

(without alignments)
1793.921 Million cell updates/sec

Title: US-10-820-820-4

Perfect score: 95

Sequence: accguuuuuucggauagugu.....aaacaagacagucuuu 95

scoring table: IDENTITY_NUC

GapOp 10.0 , GapExt: 1.0

Minimum DB seq length: 0

Maximum DB seq length: 150

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 5307602

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgtn2_6/prodata/2/pubpna/PCT07_PUBCOMB.seq: *

2: /cgtn2_6/prodata/2/pubpna/PCT06_NEW_PUB.seq: *

3: /cgtn2_6/prodata/2/pubpna/US06_NEW_PUB.seq: *

4: /cgtn2_6/prodata/2/pubpna/US05_PUBCOMB.seq: *

5: /cgtn2_6/prodata/2/pubpna/US07_NEW_PUB.seq: *

6: /cgtn2_6/prodata/2/pubpna/PUBOMB.seq: *

7: /cgtn2_6/prodata/2/pubpna/US08_NEW_PUB.seq: *

8: /cgtn2_6/prodata/2/pubpna/US09_PUBCOMB.seq: *

9: /cgtn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq: *

10: /cgtn2_6/prodata/2/pubpna/US10_PUBCOMB.seq: *

11: /cgtn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq: *

12: /cgtn2_6/prodata/2/pubpna/US10_PUBCOMB.seq: *

13: /cgtn2_6/prodata/2/pubpna/US10_PUBCOMB.seq: *

14: /cgtn2_6/prodata/2/pubpna/US10_PUBCOMB.seq: *

15: /cgtn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq: *

16: /cgtn2_6/prodata/2/pubpna/US10_PUBCOMB.seq: *

17: /cgtn2_6/prodata/2/pubpna/US10_PUBCOMB.seq: *

18: /cgtn2_6/prodata/2/pubpna/US10_PUBCOMB.seq: *

19: /cgtn2_6/prodata/2/pubpna/US10c_PUBCOMB.seq: *

20: /cgtn2_6/prodata/2/pubpna/US11c_PUBCOMB.seq: *

21: /cgtn2_6/prodata/2/pubpna/US60c_PUBCOMB.seq: *

22: /cgtn2_6/prodata/2/pubpna/US60c_PUBCOMB.seq: *

ALIGNMENTS

RESULT 1

US-10-361-028-8

Sequence 8, Application US10361028

Publication No. US2003019947A1

GENERAL INFORMATION:

APPLICANT: TAIRA, KAZUNARI

APPLICANT: WARASHINA, MASAKI

APPLICANT: KUWABARA, TOMOKO

APPLICANT: KAWASAKI, HIROKI

TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING

FILE REFERENCE: 081356/0151

CURRENT APPLICATION NUMBER: US/10/361.028

PRIOR APPLICATION NUMBER: US/09/704.525

PRIOR FILING DATE: 2000-11-03

PRIOR APPLICATION NUMBER: JP 316133/1999

PRIOR FILING DATE: 1999-11-05

NUMBER OF SEQ ID NOS: 56

SOFTWARE: PatentIn Ver. 2.1

SUMMARIES

Result No. Score % Query Length DB ID Description

1 95 100.0 95 16 US-10-361-028-8 Sequence 8, Appli

2 95 100.0 95 18 US-10-361-028-4 Sequence 4, Appli

3 74.8 78.7 88 10 US-09-974-974-5 Sequence 5, Appli

4 74.8 78.7 88 18 US-10-475-851A-3 Sequence 3, Appli

5 74.8 78.7 138 10 US-09-974-974-17 Sequence 17, Appli

6 74.8 78.7 141 16 US-10-361-028-52 Sequence 52, Appli

7 74.8 78.7 142 16 US-10-361-028-49 Sequence 49, Appli

8 74.8 78.7 142 16 US-10-361-028-50 Sequence 50, Appli

9 74.8 78.7 142 16 US-10-361-028-51 Sequence 51, Appli

10 74.8 78.7 142 16 US-10-361-028-53 Sequence 53, Appli

11 74.8 77.9 128 18 US-10-820-820-3 Sequence 3, Appli

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence: the nucleotide sequence of the transcript of the human placental tRNA^{Ala}

US-10-361-028-8

Query Match Similarity 100.0%; Score 95; DB 16; Length 95;

Best Local Similarity 100.0%; Pred. No. 4.7e-26; Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 1, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 57, Appli
Sequence 384, App
Sequence 404, App
Sequence 407, App
Sequence 30, Appli
Sequence 25, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 300, Appli
Sequence 27, Appli
Sequence 557, App
Sequence 348, App
Sequence 411, App
Sequence 442, App
Sequence 8401, App
Sequence 8437, App
Sequence 4366, App
Sequence 4385, App
Sequence 4400, App
Sequence 442, App
Sequence 442, App
Sequence 8420, App
Sequence 8435, App
Sequence 8475, App
Sequence 13, Appli
Sequence 12, Appli
Sequence 27179, App

Db 1 ACCGUUGGUUUCGGUAGUGUAGUGGUUAUCAGUUCGCCUACACGGGAAAGGUCCCCG 60
 Qy 61 UUCGAACCGGGCAACAAAGCAGTCGCTU 95
 Db 61 UUCGAACCGGGCAACAAAGCAGTCGCTU 95

RESULT 2
 US-10-820-820-4 Application US/10820820
 Sequence 4 Application US/10820820
 Publication No. US20040198689A1

GENERAL INFORMATION:
 APPLICANT: TAIRA, KAZUNARI
 APPLICANT: OHKAWA, JUN
 APPLICANT: KOSEKI, SHIORI

TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
 TITLE OF INVENTION: NUCICIC ACIDS

FILE REFERENCE: 0493-0059-00000
 CURRENT APPLICATION NUMBER: US/10-820, 820
 CURRENT FILING DATE: 2004-04-09

PRIOR APPLICATION NUMBER: US/09/763, 590
 PRIOR FILING DATE: 2001-02-26

PRIOR APPLICATION NUMBER: PCT/JP99/04718
 PRIOR FILING DATE: 1999-08-31
 PRIOR APPLICATION NUMBER: JP 10/244755
 PRIOR FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 95
 TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence 4. Application US/10820820-4

OTHER INFORMATION: Description of the transcript of human placental tRNA Val US-10-820-820-4

Query Match 100.0%; Score 95; DB 18; Length 95;
 Best Local Similarity 100.0%; Pred. No. 4.7e-26;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCGUGGUUUCGGUAGUGUAGUGGUUAUCAGGUCCGAAAGGUCCCCG 60
 Db 1 ACCGUGGUUUCGGUAGUGUAGUGGUUAUCAGGUCCGAAAGGUCCCCG 60

Qy 61 UUCGAACCGGGCAACAAAGCAGTCGCTU 95
 Db 61 UUCGAACCGGGCAACAAAGCAGTCGCTU 95

RESULT 3
 US-09-974-974-5
 Sequence 5 Application US/09974974
 Publication No. US20030013095A1

GENERAL INFORMATION:
 APPLICANT: Kazunari TAIRA
 APPLICANT: Masashi WARASHINA
 APPLICANT: Tomoko WARASHINA

TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a title of invention: target RNA by recognizing another molecule

FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/09/974, 974
 CURRENT FILING DATE: 2002-03-14
 PRIOR APPLICATION NUMBER: JP 2000-313320
 PRIOR FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5
 LENGTH: 88
 TYPE: RNA

FEATURE: ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: tRNAval promoter sequence

US-09-974-974-5
 Query Match 78.7%; Score 74.8; DB 10; Length 88;
 Best Local Similarity 91.9%; Pred. No. 2.3e-18; Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCGUUGGUUUCGGUAGUGUAGUGGUUAUCAGGUCCGAAAGGUCCCCG 60
 Db 1 ACCGUGGUUUCGGUAGUGUAGUGGUUAUCAGGUCCGAAAGGUCCCCG 60

Qy 61 UUCGAACCGGGCAACAAAGCAGTCGCTU 86
 Db 61 UUCGAACCGGGCAACTAACAAACCA 86

RESULT 5
 US-09-974-974-17
 Sequence 17 Application US/09974974
 Publication No. US20030013095A1

GENERAL INFORMATION:
 APPLICANT: Kazunari TAIRA
 APPLICANT: Tomoko WARASHINA
 APPLICANT: Masashi WARASHINA

TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a title of invention: target RNA by recognizing another molecule

FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/09/974, 974
 CURRENT FILING DATE: 2002-03-14
 PRIOR APPLICATION NUMBER: JP 2000-313320
 PRIOR FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 17
 LENGTH: 138
 TYPE: RNA

```

; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: tRNAVal T-MzL
; US-09-974-974-17

Query Match    78.7%; Score 74.8; DB 10; Length 138;
Best Local Similarity 91.9%; Pred. No. 2.5e-18; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 7; Index 0; Gaps 0;

Qy          1 ACCGUGUUGGUUCGUAGUGUAGUGGUUAUCACGUUCGCCAACCGCGAAAGGUCCCCGG 60
Db          1 ACCGUGUUGGUUCGUAGUGUAGUGGUUAUCACGUUCGCCAACCGCGAAAGGUCCCCGG 60

Qy          61 UUCCAAACCGGGCACTACAAACCA 86
Db          61 UUCCAAACCGGGCACTACAAACCA 86

RESULT 6
US-10-361-028-52
; Sequence 52, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARRASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROKO
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361, 028
; CURRENT FILING DATE: 2003-02-10
; PRIORITY APPLICATION NUMBER: US/09/704, 525
; PRIORITY FILING DATE: 2000-11-03
; PRIORITY APPLICATION NUMBER: JP 316133/1999
; PRIORITY FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 141
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
; US-10-361-028-52

Query Match    78.7%; Score 74.8; DB 16; Length 142;
Best Local Similarity 91.9%; Pred. No. 2.5e-18; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 7; Index 0; Gaps 0;

Qy          1 ACCGUGUUGGUUCGUAGUGUAGUGGUUAUCACGUUCGCCAACCGCGAAAGGUCCCCGG 60
Db          1 ACCGUGUUGGUUCGUAGUGUAGUGGUUAUCACGUUCGCCAACCGCGAAAGGUCCCCGG 60

Qy          61 UUCCAAACCGGGCACTACAAACCA 86
Db          61 UUCCAAACCGGGCACTACAAACCA 86

RESULT 7
US-10-361-028-49
; Sequence 49, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARRASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROKO
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361, 028
; CURRENT FILING DATE: 2003-02-10
; PRIORITY APPLICATION NUMBER: US/09/704, 525

Query Match    78.7%; Score 74.8; DB 16; Length 142;
Best Local Similarity 91.9%; Pred. No. 2.5e-18; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 7; Index 0; Gaps 0;

Qy          1 ACCGUGUUGGUUCGUAGUGUAGUGGUUAUCACGUUCGCCAACCGCGAAAGGUCCCCGG 60
Db          1 ACCGUGUUGGUUCGUAGUGUAGUGGUUAUCACGUUCGCCAACCGCGAAAGGUCCCCGG 60

Qy          61 UUCCAAACCGGGCACTACAAACCA 86
Db          61 UUCCAAACCGGGCACTACAAACCA 86

RESULT 8
US-10-361-028-50
; Sequence 50, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARRASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROKO
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361, 028
; CURRENT FILING DATE: 2003-02-10
; PRIORITY APPLICATION NUMBER: US/09/704, 525
; PRIORITY FILING DATE: 2000-11-03
; PRIORITY APPLICATION NUMBER: JP 316133/1999
; PRIORITY FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 142
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
; US-10-361-028-50

Query Match    78.7%; Score 74.8; DB 16; Length 142;
Best Local Similarity 91.9%; Pred. No. 2.5e-18; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 7; Index 0; Gaps 0;

Qy          1 ACCGUGUUGGUUCGUAGUGUAGUGGUUAUCACGUUCGCCAACCGCGAAAGGUCCCCGG 60
Db          1 ACCGUGUUGGUUCGUAGUGUAGUGGUUAUCACGUUCGCCAACCGCGAAAGGUCCCCGG 60

Qy          61 UUCCAAACCGGGCACTACAAACCA 86
Db          61 UUCCAAACCGGGCACTACAAACCA 86

RESULT 9
US-10-361-028-51
; Sequence 51, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:

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; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WABASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361,028
; CURRENT FILING DATE: 2003-02-10
; PRIORITY NUMBER: US/09/704,525
; PRIORITY NUMBER: JP 316133/1999
; PRIORITY NUMBER: JP 316133/1999
; PRIORITY FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 51
; LENGTH: 142
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
; OTHER INFORMATION: Sequence of CPP Rz3
US-10-361-028-51

Query Match          78.7%; Score 74.8; DB 16; Length 142;
Best Local Similarity 91.9%; Pred. No. 2.5e-18; Indels 0; Gaps 0;
Matched 79; Conservative 0; Mismatches 7; SEQ ID NO: 3
Length: 142

Qy      1 ACCGGUGGATUCCGUAGUGUAGUGUUAUCGGUCCUACCGCGAAAGGUCCGG
Db      1 UUCGAAACGGGCGGAACACAGACA 86
Qy      61 UUCGAAACGGGCGGAACACAGACA 86
Db      61 UUCGAAACGGGCGGAACACAGACA 86

RESULT 10
US-10-361-028-53
; Sequence 53, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WABASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361,028
; CURRENT FILING DATE: 2003-02-10
; PRIORITY NUMBER: US/09/704,525
; PRIORITY NUMBER: JP 316133/1999
; PRIORITY NUMBER: JP 316133/1999
; PRIORITY FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 53
; LENGTH: 142
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
; OTHER INFORMATION: Sequence of CPP Rz3
US-10-361-028-53

Query Match          78.7%; Score 74.8; DB 16; Length 142;
Best Local Similarity 91.9%; Pred. No. 2.5e-18; Indels 0; Gaps 0;
Matched 79; Conservative 0; Mismatches 7; SEQ ID NO: 3
Length: 142

Qy      1 ACCGGUGGATUCCGUAGUGUAGUGUUAUCGGUCCUACCGCGAAAGGUCCGG
Db      1 UCCGAAACGGGCGGAACACAGACA 86
Qy      61 UCCGAAACGGGCGGAACACAGACA 86
Db      61 UCCGAAACGGGCGGAACACAGACA 86

RESULT 11
US-10-820-820-3
; Sequence 3, Application US/108200820
; Publication No. US20040198689A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; FILE REFERENCE: 04053.0059-00000
; CURRENT APPLICATION NUMBER: US/10/820,820
; CURRENT FILING DATE: 2004-04-09
; PRIORITY NUMBER: US/09/763,590
; PRIORITY FILING DATE: 2001-02-26
; PRIORITY NUMBER: PCT/JP99/04718
; PRIORITY NUMBER: JP 10/244755
; PRIORITY FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 128
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: Sequence of Rz1
US-10-820-820-3

Query Match          77.9%; Score 74; DB 18; Length 128;
Best Local Similarity 93.9%; Pred. No. 4.9e-18; Indels 0; Gaps 0;
Matched 77; Conservative 0; Mismatches 5; SEQ ID NO: 3
Length: 128

Qy      1 ACCGGUGGATUCCGUAGUGUAGUGUUAUCGGUCCUACCGCGAAAGGUCCGG
Db      1 ACCGGUGGATUCCGUAGUGUAGUGUUAUCGGUCCUACCGCGAAAGGUCCGG
Qy      61 UUCGAAACGGGCGGAACACAGACA 82
Db      61 UUCGAAACGGGCGGAACACAGACA 82

RESULT 12
US-10-820-820-1
; Sequence 1, Application US/108200820
; Publication No. US20040198689A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; FILE REFERENCE: 04053.0059-00000
; CURRENT APPLICATION NUMBER: US/10/820,820
; CURRENT FILING DATE: 2004-04-09
; PRIORITY NUMBER: US/09/763,590
; PRIORITY FILING DATE: 2001-02-26
; PRIORITY NUMBER: PCT/JP99/04718
; PRIORITY FILING DATE: 1999-08-31
; PRIORITY NUMBER: JP 10/244755
; PRIORITY FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 135
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
; OTHER INFORMATION: Sequence of CPP Rz5
US-10-361-028-53

Query Match          78.7%; Score 74.8; DB 16; Length 142;
Best Local Similarity 91.9%; Pred. No. 2.5e-18; Indels 0; Gaps 0;
Matched 79; Conservative 0; Mismatches 7; SEQ ID NO: 1
Length: 142

Qy      1 ACCGGUGGATUCCGUAGUGUAGUGUUAUCGGUCCUACCGCGAAAGGUCCGG
Db      1 ACCGGUGGATUCCGUAGUGUAGUGUUAUCGGUCCUACCGCGAAAGGUCCGG
Qy      61 UUCGAAACGGGCGGAACACAGACA 86

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; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence of Rz2
US-10-820-820-1

Query Match 76.8%; Score 73; DB 18; Length 135;
Best Local Similarity 93.8%; Pred. No. 1.2e-17; Mismatches 5; Indels 0; Gaps 0;
Matched 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ACCGUNGUGUUCGUAGUGUACGGGUACCGGUCCCUAACCGGAANGGUCCCCGG 60
Oy 1 ACCGUNGUGUUCGUAGUGUACGGGUACCGGUCCCUAACCGGAANGGUCCCCGG 60
Db 61 UUCGAAACCGGCCACUACAA 81
Db 61 UUCGAAACCGGCCACUACAA 81

RESULT 13
US-10-820-820-2
; Sequence 2, Application US/10820820
; Publication No. US20040198689A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JIN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; FILE REFERENCE: 04853_0059_0000
; CURRENT APPLICATION NUMBER: US/10/820,820
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US/09/763,590
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 141
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence of Rz2
US-10-820-820-2

Query Match 73.5%; Score 69.8; DB 18; Length 149;
Best Local Similarity 97.3%; Pred. No. 2e-16; Mismatches 2; Indels 0; Gaps 0;
Matched 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACCGUNGUGUUCGUAGUGUACGGGUACCGGUCCCUAACCGGAANGGUCCCCGG 60
Oy 1 ACCGUNGUGUUCGUAGUGUACGGGUACCGGUCCCUAACCGGAANGGUCCCCGG 60
Db 61 UUCGAAACCGGCC 73
Db 61 UUCGAAACCGGCC 73

RESULT 15
US-10-820-820-7/c
; Sequence 7, Application US/10820820
; Publication No. US20040198689A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JIN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; FILE REFERENCE: 04853_0059_0000
; CURRENT APPLICATION NUMBER: US/10/820,820
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US/09/763,590
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of an
; OTHER INFORMATION: antisense oligonucleotide linker
US-10-820-820-7

Query Match 70.3%; Score 66.8; DB 18; Length 113;
Best Local Similarity 71.4%; Pred. No. 2.6e-15; Mismatches 50; Conservative 18; Mismatches 2; Indels 0; Gaps 0;
Matched 50; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ACCGUNGUGUUCGUAGUGUACGGGUACCGGUCCCUAACCGGAANGGUCCCCGG 60
Oy 1 ACCGUNGUGUUCGUAGUGUACGGGUACCGGUCCCUAACCGGAANGGUCCCCGG 60
Db 71 ACCGTTGTTCCGTAGTGTAGTGGTATCAGTTCGCCTAACCGSGAAAGTCCCGG 12
Db 61 UUCGAAACCG 70
Oy 61 UUCGAAACCG 70
Db 11 TTGGAATCTCG 2

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Tue Feb 22 13:22:42 2005

us-10-820-820-4.rnpb

Page 6

Search completed: February 18, 2005, 23:26:29
Job time : 314 secs

GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model

Run on: February 18, 2005, 21:34:12 ; Search time 2446 Seconds
(Without alignments) 1585.523 Million cell updates/sec

Title: US-10-820-820-4
Perfect score: 95
Sequence: 1 accgguuuuucggauugu.....aaacaagacagucuuu 95

Scoring table: IDENTITY_NUC
GapOp 10⁻⁰, GapExt 1.0

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA Main: *

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2: /cgn2_6/ptodata/1/pna/PC7US2 COMB. seq: *
3: /cgn2_6/ptodata/1/pna/PC7US3 COMB. seq: *
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8: /cgn2_6/ptodata/1/pna/US082 COMB. seq: *
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24: /cgn2_6/ptodata/1/pna/US096 COMB. seq: *
25: /cgn2_6/ptodata/1/pna/US095C COMB. seq: *
26: /cgn2_6/ptodata/1/pna/US096A COMB. seq: *
27: /cgn2_6/ptodata/1/pna/US096B COMB. seq: *
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29: /cgn2_6/ptodata/1/pna/US096D COMB. seq: *
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38: /cgn2_6/ptodata/1/pna/US098D COMB. seq: *
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46: /cgn2_6/ptodata/1/pna/US100A COMB. seq: *
47: /cgn2_6/ptodata/1/pna/US100B COMB. seq: *
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67: /cgn2_6/ptodata/1/pna/US109H COMB. seq: *
68: /cgn2_6/ptodata/1/pna/US109I COMB. seq: *
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77: /cgn2_6/ptodata/1/pna/US6009 COMB. seq: *
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81: /cgn2_6/ptodata/1/pna/US6013 COMB. seq: *
82: /cgn2_6/ptodata/1/pna/US6014 COMB. seq: *
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98: /cgn2_6/ptodata/1/pna/US6030 COMB. seq: *
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106: /cgn2_6/ptodata/1/pna/US6038 COMB. seq: *
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110: /cgn2_6/ptodata/1/pna/US6042 COMB. seq: *
111: /cgn2_6/ptodata/1/pna/US6043 COMB. seq: *
112: /cgn2_6/ptodata/1/pna/US6044 COMB. seq: *
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114: /cgn2_6/ptodata/1/pna/US6046 COMB. seq: *
115: /cgn2_6/ptodata/1/pna/US6047 COMB. seq: *
116: /cgn2_6/ptodata/1/pna/US6048 COMB. seq: *
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124: /cgn2_6/prodata/1/pna/US6054_COMBO.seq:*
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126: /cgn2_6/prodata/1/pna/US6056_COMBO.seq:*
127: /cgn2_6/prodata/1/pna/US6057_COMBO.seq:*
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129: /cgn2_6/prodata/1/pna/US6059_COMBO.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score or the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	
1	95	100.0	95	32	US-09-704-525-8	
2	95	100.0	95	32	US-09-718-098-15	
3	95	100.0	95	53	US-10-361-028-8	
4	95	100.0	95	63	US-10-820-820-4	
5	74.8	78.7	88	28	US-09-623-932-3	
6	74.8	78.7	88	28	US-09-623-932A-3	
7	74.8	78.7	88	44	US-09-974-974-5	
8	74.8	78.7	88	55	US-10-475-851A-3	
9	74.8	78.7	88	56	US-10-532-380-1	
10	74.8	78.7	91	32	US-09-718-098-16	
11	74.8	78.7	128	28	US-09-623-932A-20	
12	74.8	78.7	135	28	US-09-623-932A-18	
13	74.8	78.7	137	45	US-09-984-198A-2	
14	74.8	78.7	138	44	US-09-974-974-17	
15	74.8	78.7	141	32	US-09-104-525-52	
16	74.8	78.7	141	53	US-10-361-028-52	
17	74.8	78.7	142	32	US-09-704-525-49	
18	74.8	78.7	142	32	US-09-704-525-50	
19	74.8	78.7	142	32	US-09-704-525-51	
20	74.8	78.7	142	32	US-09-704-525-53	
21	74.8	78.7	142	53	US-10-361-028-49	
22	74.8	78.7	142	53	US-10-361-028-50	
23	74.8	78.7	142	53	US-10-361-028-51	
24	74.8	78.7	142	53	US-10-361-028-53	
25	74	77.9	128	63	US-10-820-820-3	
26	73	76.8	135	63	US-10-820-820-1	
27	73	76.8	141	63	US-10-820-820-2	
28	69.8	73.5	149	63	US-10-820-820-5	
c	29	66.8	70.3	113	63	US-10-820-820-7
c	30	66	69.5	110	63	US-10-820-820-6
c	31	63	66.3	2	PCT-US03-40292-57	
c	32	63	66.3	64	62 US-10-738-642-57	
c	33	61.8	65.1	69	16 US-09-047-923-3336	
c	34	61.8	65.1	69	25 US-09-440-765-43340	
c	35	41	43.2	73	114 US-60-445-574-118	
c	36	40	42.1	73	79 US-60-615-573-3	
c	37	38.8	40.8	129	22 US-09-450-965-3090	
c	38	38.8	40.8	129	62 US-10-724-922-3090	
c	39	38.4	40.4	73	79 US-60-615-573-10841	
c	40	38.4	40.4	138	22 US-09-450-965-2465	
c	41	38.4	40.4	138	62 US-10-724-922-2465	
c	42	35.2	37.1	73	64 US-10-857-625-384	
c	43	35.2	37.1	73	64 US-10-857-625-404	
c	44	35.2	37.1	73	64 US-10-857-625-407	
c	45	37.1	73	64	US-10-859-198-3224	

ALIGNMENTS


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RESULT 7
; Sequence 5, Application US/09974974
; GENERAL INFORMATION:
; APPLICANT: Kazunari Taira
; APPLICANT: Tomoko WASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,974
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 88
; TYPE: RNA
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: tRNAval promoter sequence
; US-09-974-974-5

Query Match 78.7%; Score 74.8; DB 44; Length 88;
Best Local Similarity 91.9%; Pred. No. 1.8e-17; Mismatches 7; Indels 0; Gaps 0;
Matches 79; Conservative 0; MisMatches 7; Indels 0; Gaps 0;

Qy 1 ACCGGUGUCCGUAGUGAGUGGUAUCACGUUCGCCAACCGGAAGGUCCCCGG 60
Db 1 ACCGGUGUCCGUAGUGAGUGGUAUCACGUUCGCCAACCGGAAGGUCCCCGG 60

Qy 61 UUCAAACCGGGGGAAACAAAGACA 86
Db 61 UUCAAACCGGGGGAAACAAAGACA 86

RESULT 8
; Sequence 3, Application US/10475851A
; GENERAL INFORMATION:
; APPLICANT: Taira, Kazunari
; APPLICANT: WARASHINA, Tomoko
; APPLICANT: KAWASAKI, Hiroaki
; APPLICANT: HARA, Toshihumi
; APPLICANT: NOZAWA, Iwao
; TITLE OF INVENTION: Novel Maxizyme
; FILE REFERENCE: P24426
; CURRENT APPLICATION NUMBER: US/10/475,851A
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/JP02/04322
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-974-974-5

Query Match 78.7%; Score 74.8; DB 44; Length 88;
Best Local Similarity 91.9%; Pred. No. 1.8e-17; Mismatches 7; Indels 0; Gaps 0;
Matches 79; Conservative 0; MisMatches 7; Indels 0; Gaps 0;

Qy 1 ACCGGUGUCCGUAGUGAGUGGUAUCACGUUCGCCAACCGGAAGGUCCCCGG 60
Db 1 ACCGGUGUCCGUAGUGAGUGGUAUCACGUUCGCCAACCGGAAGGUCCCCGG 60

Qy 61 UUCAAACCGGGGGAAACAAAGACA 86
Db 61 UUCAAACCGGGGGAAACAAAGACA 86

RESULT 9
; Sequence 1, Application US/10512386
; GENERAL INFORMATION:
; APPLICANT: NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR STEM-LOOP RNA MOLECULES HAVING RNAI EFFECT
; FILE REFERENCE: GTU-A023YIP
; CURRENT APPLICATION NUMBER: US/10/512,386
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: JP 2002-127089
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: JP 2003-4705
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/449,860
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-512-386-1

Query Match 78.7%; Score 74.8; DB 56; Length 88;
Best Local Similarity 91.9%; Pred. No. 1.8e-17; Mismatches 7; Indels 0; Gaps 0;
Matches 79; Conservative 0; MisMatches 7; Indels 0; Gaps 0;

Qy 1 ACCGGUGUCCGUAGUGAGUGGUAUCACGUUCGCCAACCGGAAGGUCCCCGG 60
Db 1 ACCGGUGUCCGUAGUGAGUGGUAUCACGUUCGCCAACCGGAAGGUCCCCGG 60

Qy 61 UUCAAACCGGGGGAAACAAAGACA 86
Db 61 UUCAAACCGGGGGAAACAAAGACA 86

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RESULT 10
; Sequence 16, Application US/09718098
; GENERAL INFORMATION:
; APPLICANT: TANAKA, MANAMI
; TITLE OF INVENTION: RIBOZYMES TARGETING BRADETON TRANSCRIPTS AND USE
; FILE REFERENCE: 091356/0155
; CURRENT APPLICATION NUMBER: US/09/718,098
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: A mutant tRNA(Val)
; OTHER INFORMATION: promoter
; US-09-718-098-16

Query Match 78.7%; Score 74.8; DB 32; Length 91;
Best Local Similarity 70.9%; Pred. No. 1.8e-17; Mismatches 7; Indels 0; Gaps 0;
Matches 61; Conservative 18; MisMatches 7; Indels 0; Gaps 0;

Qy 1 ACCGGUGUCCGUAGUGAGUGGUAUCACGUUCGCCAACCGGAAGGUCCCCGG 60
Db 1 ACCGGUGUCCGUAGUGAGUGGUAUCACGUUCGCCAACCGGAAGGUCCCCGG 60

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RESULT 11
US-09-623-932A-20
Sequence 20, Application US/09623932A
GENERAL INFORMATION:
APPLICANT: Taisho Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Nucleic acid enzyme having allosteric RNA-cleaving activity on target sequence
FILE REFERENCE: 060764
CURRENT APPLICATION NUMBER: US/09/623, 932A
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: JP 60969/1998
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: JP 311098/1998
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: PCT/JP99/01187
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 128
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Component of tRNAval-MzR
US-09-623-932A-20

Query Match Similarity 78.7%; Score 74.8; DB 28; Length 128;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGCGUUGGUUCGGUAGUGUAGUGGUACGUGUACGCCUAACCGGAAGGUCCGG 60
Db 1 ACCGUGUUGGUUCGGUAGUGUAGUGGUACGUGUACGCCUAACCGGAAGGUCCGG 60

QY 61 UUCGAACCGGGCACUCAAAACCA 86
Db 61 UUCGAACCGGGCACUCAAAACCA 86

RESULT 12
US-09-622-932A-18
Sequence 18, Application US/09622932A
GENERAL INFORMATION:
APPLICANT: Taisho Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Nucleic acid enzyme having allosteric RNA-cleaving activity on target sequence
FILE REFERENCE: 060764
CURRENT APPLICATION NUMBER: US/09/622, 932A
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: JP 60969/1998
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: JP 311098/1998
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: PCT/JP99/01187
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
LENGTH: 135
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Component of tRNAval-MzL

Query Match Similarity 78.7%; Score 74.8; DB 28; Length 135;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ACCGUGUUGGUUCGGUAGUGUAGUGGUACGUGUACGCCUAACCGGAAGGUCCGG 60
Db 1 ACCGUGUUGGUUCGGUAGUGUAGUGGUACGUGUACGCCUAACCGGAAGGUCCGG 60

QY 61 UUCGAACCGGGCACUCAAAACCA 86
Db 61 UUCGAACCGGGCACUCAAAACCA 86

RESULT 13
US-09-984-198A-2
Sequence 2, Application US/09984198A
GENERAL INFORMATION:
APPLICANT: Taira, Kazunari
TITLE OF INVENTION: METHODS FOR SELECTING HIGHLY FUNCTIONAL NUCLEIC ACID MOLECULES WITHIN CELLS

FILE REFERENCE: 4353.0080-00
CURRENT APPLICATION NUMBER: US/09/984, 198A
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 311347/2000
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
LENGTH: 137
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence of tRNA-Luc GUA Rz
NAME/KEY: misc_feature
LOCATION: (70)..(91)
OTHER INFORMATION: 22mer random sequence

US-09-984-198A-2

Query Match Similarity 78.7%; Score 74.8; DB 45; Length 137;
Best Local Similarity 91.9%; Score No. 2e-17; DB 45; Length 137;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGCGUUGGUUCGGUAGUGUAGUGGUACGUGUACGCCUAACCGGAAGGUCCGG 60
Db 1 ACCGUGUUGGUUCGGUAGUGUAGUGGUACGUGUACGCCUAACCGGAAGGUCCGG 60

QY 61 UUCGAACCGGGCACUCAAAACCA 86
Db 61 UUCGAACCGGGCACUCAAAACCA 86

RESULT 14
US-09-974-974-17
Sequence 17, Application US/09974974
GENERAL INFORMATION:
APPLICANT: Kazunari TAIRA
APPLICANT: Masashi WAKASHINA
TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a target RNA by recognizing another molecule

FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/974, 974
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: JP 2000-313320
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 138
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial sequence: tRNAval-T-MzL

Query Match Similarity 78.7%; Score 74.8; DB 28; Length 135;
Best Local Similarity 91.9%; Score No. 2e-17; Length 135;
SEQ ID NO 17
LENGTH: 138
TYPE: RNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial sequence: tRNAval-T-MzL

US-09-974-974-17

Query Match Similarity 78.7%; Score 74.8; DB 44; Length 138;
 Best Local Similarity 91.9%; Pred. No. 2e-17; Mismatches 7; Indels 0; Gaps 0;
 Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACCGUGGUUUCGGGAAACAAAGACA 86
 Db 1 ACCGUGGUUUCGGGAAACAAAGACA 86
 Qy 61 UUCGAACCGGGCACUACAAACCA 86
 Db 61 UUCGAACCGGGCACUACAAACCA 86

RESULT 15

US-09-704-525-52

; Sequence 52, Application US/09704525
 ; GENERAL INFORMATION:
 ; APPLICANT: TAITRA, KAZUNARI
 ; APPLICANT: WARASHINA, MASAKI
 ; APPLICANT: KUMABARA, TOMOKO
 ; APPLICANT: KAWASAKI, HIROAKI
 ; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
 ; PILE REFERENCE: 81356/0151
 ; CURRENT APPLICATION NUMBER: US/09/704,525
 ; CURRENT FILING DATE: 2000-11-03
 ; PRIOR APPLICATION NUMBER: JP 316133/1999
 ; PRIOR FILING DATE: 1999-11-05
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 52
 ; LENGTH: 141
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
 ; OTHER INFORMATION: Sequence of CPP Rz4
 ; US-09-704-525-52

Query Match Similarity 78.7%; Score 74.8; DB 32; Length 141;
 Best Local Similarity 91.9%; Pred. No. 2e-17; Mismatches 7; Indels 0; Gaps 0;
 Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACCGUGGUUUCGGGAAACAAAGACA 86

Db 1 ACCGUGGUUUCGGGAAACAAAGACA 86
 Qy 61 UUCGAACCGGGCACUACAAACCA 86
 Db 61 UUCGAACCGGGCACUACAAACCA 86

Search completed: February 18, 2005, 23:15:43
 Job time : 2448 secs